Quantitative approaches to kinship terminology evolution

By

Sam Passmore

Department of Anthropology and Archaeology
University of Bristol

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Abstract

Diversity in kinship is higher in humans than in any other species (Chapais, 2009). Human kinship does not only entail reproduction, but divides relatives into categories which convey important, culturally specific information (Jones, 2010; Parkin, 2012). These cultural categories of kin are expressed linguistically in kinship terminology, a system of words for relatives. Despite the variety in how kinship is enacted, some theorists have declared cross-cultural organisation of kinship terminology to be constrained to very few types only ten or so (Godelier, 2012, pg. 180).

In this thesis, I examine kinship terminology diversity using evolutionary anthropological theory. I applied evolutionary methods to question the universality of existing theories; I developed a global kinship terminology database and projected observed diversity into a morphospace to conceptually and quantitatively test for universal patterns of kinship terminology; and tested cultural-evolutionary predictions of kin categorisation on behaviour.

Chapter 2 used phylogenetically-controlled methods to test eighteen hypothesis between kinship typology and social structure in three language families (Austronesian, Bantu, and Uto-Aztecan), finding little co-evolutionary support between and considerable lineage specific trends. This highlighted the need for rigorous analysis of existing ideas and the lack of diversity captured in the existing typology.

To establish the true extent of kinship terminology diversity, I build (with colleagues) a database of 1,022 kinship terminologies, Kinbank (chapter 3). Using this global sample, I conceptualised a morphospace approach to kinship terminology diversity, named kinspace, incorporating cultural, biological, and cognitive constraints (chapter 4). I then quantitatively approximated kinspace to establish a new typology and proposed theories of terminological change from the common structures (chapter 5).

Beyond the macro- and structural- properties of kinship terminology are how they are enacted by individuals. The chapter 6 found that linguistic categorisation of kin influences cooperative behaviour, by comparing economic decisions between languages with different kin terminology (American-English and Hindi).

This thesis established the importance of evolutionary theory in understanding the relationship between language and social structure; in understanding the constraints on diversity imposed from cultural, biological, and cognitive pressure; and finally exploring the impact of macro-level structures on individual behaviour.

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Author's declaration

I declare that the work in this dissertation was carried out in accordance with the requirements of the University's Regulations and Code of Practice for Research Degree Programmes and that it has not been submitted for any other academic award. Except where indicated by specific reference in the text, the work is the candidate's own work. Work done in collaboration with, or with the assistance of, others, is indicated as such. Any views expressed in the dissertation are those of the author.

SIGNED: .....SAM PASSMORE..... DATE: .....14TH SEPTEMBER 2020.....

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Glossary

affine A relative linked by marriage.

collateral kin Kin who are related off a direct line of descent (e.g. parent's siblings).

consanguine A relative linked by blood. Also known as a genealogical relative.

cross kin When a relationship between ego and ego's parent's opposite-gender sibling (and relatives extending from this link) are linguistically distinct from a same-gender sibling. As seen in Iroquois type.

ego The central figure within a kinship system, from which all relationships extend.

emic The language-internal logic for describing a particular concept.

etic Describing a cultural concept using an external referent for comparison.

exogamy The custom of joining a group other than your own after marriage.

kin term The cultural-linguistic word used to describe a relative, or group of relatives.

kin type An analytical concept defining a relative by their genealogical or marital ties.

lineal kin Kin who form a direct line of decent to ego (e.g. father, father's father, father's father's father etc).

monogamy When individuals can only be married to one person at a time.

niblings The children of ego's siblings.

parallel kin Kin who are related through parent's same-sex siblings.

polygyny When men can marry multiple women. A specific subset of this is sororal polygyny, where a man will be married to multiple sisters.

Chapter 1

Kinship, Kinship Terminology, and Anthropology

Diversity in kinship is higher in humans than in any other species (Chapais, 2009). In many primate species, kinship ties rely on mother-child bonds, which are built through a combination of familiarity (being with the mother and relatives since birth) and to a lesser extent, phenotypic cues (looks, smells, sounds) (Silk, 2009). Human kinship, on the other hand, often branches through countless generations (e.g. great-great-grandparents), can include relatives that are not related through blood (step-parents, or even uncles and aunts), and imposes a privileged cultural order over the network of familial connections (Parkin, 1997). The cultural order of kinship varies considerably between societies, influencing the expectations and behaviour between relatives.

Consider a young boy born in England visiting his mother's brother - or *uncle*. He is expected to respectfully offer his uncle the last piece of cake, while graciously accepting an unwanted third cup of tea from their mother's brother's daughter - or *cousin*. A stereotypical white, English family portrays an uncle as a wise, friendly, and trustworthy relative to which the young boy should show deference, and the relationship between cousins is amicable, contact is potentially infrequent, and any relationship between them is strictly non-sexual. However, if this same scenario is played out amongst Lau Fijians, the relationships between these individuals are fundamentally changed. Kinship in Lau Fiji is defined by cross kin, that is, a phenomena which gives special cultural significance to kin who are related through their parent's opposite-gender siblings (mother's brother or father's sister). In Lau Fiji, a mother's brother and sister's son often have a *vasu* relationship (Walter, 1979), which places the young boy in a ritually higher status than his mother's brother. Vasu relationships give the young boy appropriation rites over the mother's brother's property, meaning the cake should preferentially go to the young boy (although the extent to which this norm is enforced varies throughout the Fijian

islands Hocart, 1923). Cross-cousins (children of your parent's opposite gender sibling), have a joking relationship, or *veitavaleni*, which is described as relationship of mutual disrespect, and in the case of Lau Fijian, cross-cousins are preferred marriage partners (Arno, 1976; Parkin, 1993). A joking relationship often descends into a public, verbal performance outlining the failings of each participant where all criticisms must be taken in good faith. Within a joking relationship, no topic of conversation is off-limits and no offence can be made between the boy and his cross-cousin (Parkin, 1993). The offering of tea from a female cross-cousin is then unlikely to occur in the first place in Lau Fijian society, and perhaps offered with a sharp tongue if it does.

The difference in how the scenario plays out within a nuclearised family system (nuclear being a monogamous couple and their children) in England and the cultural implications of a crossed relationships in Lau Fiji, emphasises the cultural differences in kinship-based relationships between the groups. Unlike most other species, human kinship does not only entail the reproductive relationship between parents and children, but conveys important culturally-specific information such as who people should or should not marry (Trautmann & Whitely, 2012), where people should live (Fortunato & Jordan, 2010), how resources are inherited (Holden & Mace, 2003), who provides child care (Danziger, 1993), and how how relationships should be enacted (Parkin, 1993). Over time, these norms create lasting patterns within and between groups, for example: prescribed inter-group marriage helps form alliances (particularly during wartime, e.g. Macfarlan et al., 2018), norms of where newly weds should live create flows of people, taking with them different technologies (e.g. Buckley & Boudot, 2017) and different languages (e.g. Lansing et al., 2017; Pakendorf, Gunnink, Sands, & Bostoen, 2017), while the inheritance of land or wealth influences the structure of society and power within communities and between men and women (e.g. Holden & Mace, 2003).

The cultural representation of kin is expressed linguistically in the kinship terminology of a particular group. A kinship terminology is a system of words that designate relationships between kin (figure 1.1; Godelier, 2012). The organisation of a kinship terminology is the phenotypic expression of the effects of reproduction, the cultural meaning of kin, and cognitive and linguistic constraints on language (Jones, 2010; Kemp & Regier, 2012). Kinship terminologies allow individuals to communicate their position within a community (Godelier, 2012), and consequentially coordinate expectations of behaviour (Gerkey & Cronk, 2010). By studying how the diversity of kinship terminology arises we inform our picture of the human past and deepen the understanding of modern cultural diversity. The study of this linguistic phenomenon allows us to parse the relationship between cultural definitions of kin and biologically defined reproductive networks, and how cultural categorisation of kin relates to social norms of behaviour.

The centrality of kinship to every human life creates a feeling of normalcy to any particular condition, often making alternative constructions of kinship potentially unfathomable, foreign,

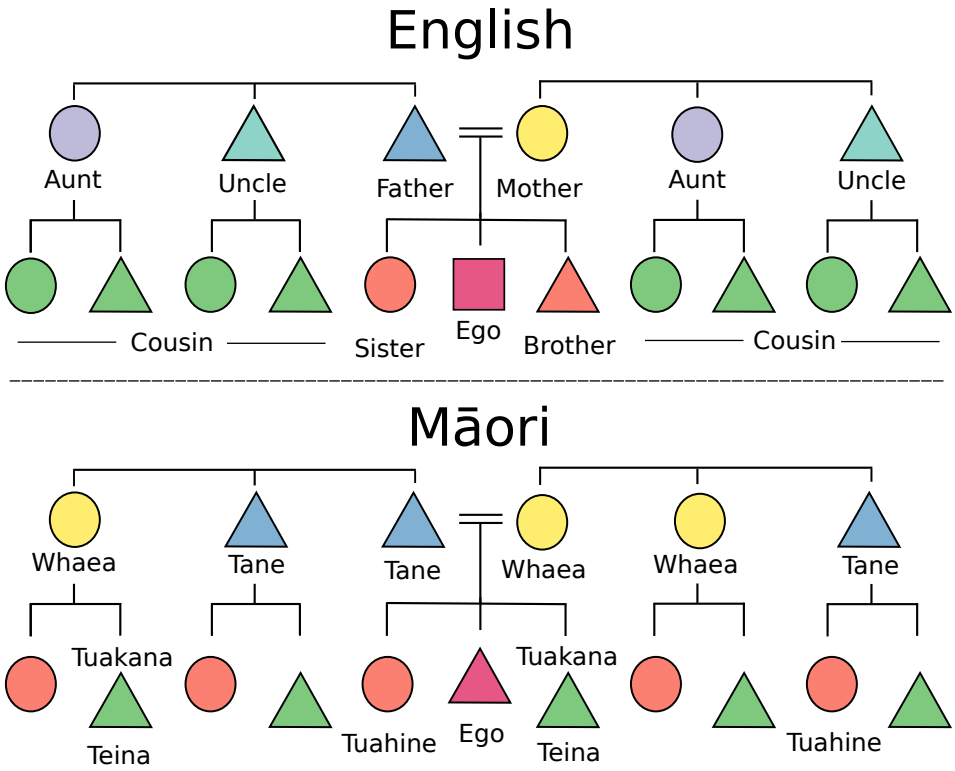

Figure 1.1: This figure shows a common depictions of kinship terminology in English and Māori. Kin types are depcited by shapes and genealogically defined connecting lines, where circles are women, triangles are men. Colours represent equivalent kin terms: for example in English, all cousins are green. Marriage is indicated by parallel lines. As an example of terminology diversity, English is contrasted with Māori. In Māori, kin terms depend on the sex of speaker, hence ego is now specified as a triangle. Kin terms for parents extend to their parent's siblings. Sibling and cousin terms are all equivalent, and males distinguish their older brother (*tuakana*) from their younger brother (*teina*), with a single term for sisters (*tuahine*). Females distinguish relative age in their sisters, and have a single word for *brother*.

and thus for the anthropologist, a domain of interest. The omnipresence of kinship terminology in all human society makes kinship terminology one the few universal anthropological domains, and exhibits wide, but not unconstrained diversity. For example: The nuclear family is the central economic unit and customary definition of a family in most societies in mid-Western Europe (Heady, 2011). The wide-spread and lay belief that the nuclear family is reasoned to reflect "natural" connections derived from reproduction but is more likely to reflect cultural changes imposed by the spread of the Catholic church in Europe during the middle ages (Schulz, Bahrami-Rad, Beauchamp, & Henrich, 2019). In fact, the nuclear family reflects only a tiny proportion of kinship structures in the world (as will be explored throughout this thesis). Amongst Māori, the primary economic unit is whānau (Best, 1924). One whānau might consist of two brothers, a sister, their children, grandchildren, and potentially great-grandchildren, and have been seen to contain upward of 90 relatives. Cultural differences in the definition of kin

(e.g. the importance of descent practices) changes how kin interact with each other (Parkin, 1993), and differences in marriage customs (e.g. who is marriageable, where do married couples live) change how families interact with each other (Lansing et al., 2017). The combination of descent, residence, and marriage practices guide and coordinate connections within and between communities. Where in one society a child might have one mother and father, another might have many socially defined parents. Where one group might separate siblings from cousins, another might only divide them by gender, and another might group all relatives of a generation under one word.

While variation in kinship terminology is higher than popular belief may assume, diversity is also remarkably constrained relative to theoretical possibility (Kemp & Regier, 2012). There are 4,140 possible ways to organise a set of eight sibling terms, but recurring patterns are frequent between unrelated languages (Nerlove & Romney, 1967). For example: Japanese distinguishes siblings based on gender and relative age (elder brother: ani; elder sister: ane; younger brother: otōto; younger sister: imōto), but so does Bengali (Bangladesh); Badimaya (Australia); Zulu (South Africa); and 226 other languages from 43 different language families (as will be discussed further in chapter 3 and 5). On this basis, it has been argued that the recurring patterns of kinship terminology must reflect underlying and universal restrictions on the diversity of kinship structures, and therefore on human society (Murdock, 1949).

The primary hypothesis for the recurrence of patterns in kinship terminology is due to the constraints imposed by social structure (Godelier, 2012). Specifically, the culturally specific rules surrounding: which family lineages are important (descent patterns); where newly-wed couples live after marriage (post-marital residence); which kin can and cannot marry, how that marriage is arranged, and the financial implications of the arrangement (marriage rules); and how wealth is inherited (inheritance rules) (Jones, 2010). Each of these domains are reflected in the categorisation of kin, and combine to create a kinship terminology which is hypothesised to coordinate behaviour between kin by encouraging behaviour that aligns with local cultural norms (Gerkey & Cronk, 2010).

In order to understand the underlying cross-cultural structures that create the recurring patterns of kinship terminology (i.e. social structure), anthropologists have historically reduced terminology to a type (Lowie, 1928; Morgan, 1871; Murdock, 1949). A type highlights the principles underlying the construction of terminology and designate the configuration of terms (Godelier, 2012). A set of types is referred to as a typology (Song, 2018). Reducing diversity to a typology helps remove culturally specific noise in comparative analysis, and highlights variation that is of theoretical interest - in this case, reducing kinship terminology to principles that reflect patterns of social structure (Kronenfeld, 2006). With restricted diversity and recurring structural patterns, it is logical to assume that diversity in kinship terminology could be divided into tractable categories that are descriptive of diversity, and predictive of social structure.

Much of the foundational work linking kinship terminology to social structure was per-

formed using typology (e.g. Goody, 1970). Typology is used to study the relationship between terminology and social structure for two main reasons. Firstly, typology converts the complexity of linguistic data into a numerical format amenable to statistical analysis. And secondly, as above, it remove culturally specific noise that can disguise an underlying relationship. However, as the depth of the ethnographic record increased, and cross-cultural information became more accessible, researchers have lamented how existing typologies lacked descriptive and predictive power (Chapter 2; Godelier, 2012), resulting in new typologies (Lowie, 1928; Murdock, 1949), extended typologies (Lounsbury, 1964), and calls to start dividing organisations from scratch (Kronenfeld, 2006). After 150 years of study, the field is yet to arrive at a unified consensus on how to divide kinship terminology variation (Parkin, 1997).

This thesis will argue that much of the disagreement in kinship terminology typology is due to an underestimation of diversity. Famously, kinship specialists declared the cross-cultural diversity in kinship terminology is constrained to "very few types ... only ten or so", despite an exponentially larger set of possibilities (Godelier, 2012, p. 180). When considering the significant diversity in kinship organisation (i.e. residence practices, marriage practice, inheritance, etc.), and the belief that kinship terminology conveys this information, it is curiously dissonant to predict that there should be so few kinship terminologies across all societies. By using an evolutionary framework, new data, and new methods, this thesis aims to establish the utility of existing typology, and assess the validity of existing typology by quantifying observed diversity and identifying recurring kinship structures from the bottom, up.

The remainder of this introductory chapter reviews the longstanding and changing preoccupation of kinship to the discipline of anthropology, with specific reference to kinship terminology and typology. Some kinship terminology concepts are defined that will aid in the discussion throughout the thesis, before finally moving into a critique of the most commonly used kinship typology and a description of some more recent approaches to describe kinship terminology.

1.1 Kinship and Kinship terminology

Kinship is a cardinal topic in anthropology because it is thought to be a driving force behind many aspects of societal organisation (Murdock, 1949). Difference in societal organisation are in turn thought to be a major driver in cultural diversity, influencing a range of social features, from macro-level differences in the development of religion (Watts, Sheehan, Atkinson, Bulbulia, & Gray, 2016), to mirco-level diversity in psychological traits (Smaldino, Lukaszewski, Rueden, & Gurven, 2019).

From early in anthropological literature was a general belief that early human groups were largely kin-based, making kin and kinship the unifying domain between individuals in a so-

ciety.[1] In the absence of states and government, extended kinship ties become the primary connections between individuals, and ultimately, between groups. For example: an early structuralist understanding of society emphasised the exchange of sisters as wives between groups as a mechanism for creating extended kin networks (Lévi-Strauss, 1969). The routine exchange of sisters created a cycle of solidarity between groups and an extended network of kin from who groups and individuals could rely on. The centrality of kinship to social structure then suggested that difference in kinship may be a leading cause in cross-cultural diversity.

Evolutionary anthropologists, and evolutionary behaviourists latched onto the idea of kinship as a central structure in human interaction (e.g. Chagnon, Irons, & Cronk, 2000). Cultural variation in kinship organisation in evolutionary anthropology and human behavioural evolution are proposed to reflect an adaptive response to the ecological conditions. For example: prescriptive marriage rules may mediate mate-competition (Chagnon, 2000); kin-relationships coordinate hunting efforts (Nolin, 2011); and raising unrelated children may increase future reproductive opportunities (J. B. Lancaster & Kaplan, 2000). The importance of kin to the structure of society creates a pressure to convey the expectations of how kin should behave towards each other to maintain within group harmony. Kinship terminology is often proposed as a mechanism which echoes the fitness interdependence between kin arising from the ecological conditions, and coordinates kin-oriented behaviour to improve group cohesion (Cronk, Steklis, Steklis, van den Akker, & Aktipis, 2018; Gerkey & Cronk, 2010). Using a linguistic strategy to mark kin in line with social norms provides a cue to individuals on what expectations and behaviour they should expect and are expected to show. This is particularly salient when encouraging alloparenting, where mothers will use linguistic strategies to impose expectations of care from other, sometimes unrelated, adults on her children (Hrdy, 2009). In this case, kin terms are utilised to manufacture closer relationship ties and mark those individuals who are suitable for care. The linguistic marking strategy is often extends to which individuals are suitable for marriage (Lounsbury, 1964) and who is part of your descent group (or who is not) (Trautmann & Whitely, 2012).

The use of kin terms as linguistic cues highlights that kinship terminology are not a topic of interest in their own right, but a tool from which to infer historical differences in social life in the absence of other information, and equally, how they continue to inform behaviour of individuals in contemporary society. Linguists (e.g. Blust et al., 1980; Ehret, 2011), and anthropologists (e.g. Cronk et al., 2018) have relied on the presumed link between typology and social structure in order to paint a picture of how our ancestors lived and navigated their world (Blust et al., 1980; Ehret, 2011); to understand the relationships and social networks our ancestors used to give rise to contemporary diversity (Allen, 2009); and to feel an intimacy with the lives that come before our own (Allen, 2009; Blust et al., 1980; Cronk et al., 2018; Ehret, 2011).

[1] Previously, it had been suggested that this was the case for both hunter-gatherer groups and early farmers, but recent research has shows hunter-gather groups consist of a more diverse group of individuals than only genealogical kin (K. R. Hill et al., 2011)

But, the strength of the correlation between kinship terminology and social structure is still an open question, and one this thesis will explore. If we can unravel the relationship between social, biological, cognitive, and historical processes that interact to establish contemporary diversity kinship terminology, we can begin to understand how cross-cultural variability in kin categorisation explains evolutionary, social, and linguistic hypotheses.

1.1.1 Studying kinship terminology

Within anthropology there are two main approaches to studying kinship terminology, namely, etic and emic. An etic approaches defines a cultural phenomena by an external and language independent metric. Emic approaches unlock each language's inner logic by taking locally meaningful categories of terms as fundamental (Evans, 2010). This thesis will utilise an etic approach, which uses a genealogical grid of relatives as a prototypical referent from which to compare societies. The genealogical grid links relatives through reproductive and marital ties, also distinguishing by relative age and by gender. The cultural categorisation of kin are laid atop the genealogical grid, creating a prototypical referent from which societies can be compared.

The comparative nature of the etic approach is its main strength, and is a hallmark of cognitive anthropology. Prototypical referents have been used in domains such as colour naming (Berlin & Kay, 1991), and body part naming (Majid, Jordan, & Dunn, 2015). In colour naming, the etic approach revealed a universal trajectory of evolution in colour naming systems (Berlin & Kay, 1991; Haynie & Bowern, 2016; Kay & Maffi, 1999), wheres in body parts, the prototypical referent allowed the quantification and comparison of body part naming and highlighted partonomic differences in the understanding of the body (Enfield, Majid, & van Staden, 2006). An etic approach in kinship terminology has allowed macro-level comparison of kinship terminology resulting in the discovery of recurring terminology structure (Goodenough, 1956; Greenberg, 1949; Kronenfeld, 2006; Morgan, 1851; Murdock, 1949; Scheffler, 1967); the inference of historical kinship organisation (Allen, 2009; Blust et al., 1980; Hage, 1999; Jordan, 2011; Shimkin, 1941); in identifying the explicit links of terminology to social structure (Goody, 1970; Lounsbury, 1964; Murdock, 1949; Trautmann & Whitely, 2012); and identifying the limits of terminological structure (Epling, Kirk, & Boyd, 1973; Lowie, 1928; Nerlove & Romney, 1967).

While the division of relatives onto a genealogical grid makes logical and comparative sense, each individual category does not necessarily have any cultural meaning. For example, in English, father's older brother is not category that is denoted linguistically, but it is a category within the etic grid. The alternative emic approach, which in kinship studies is also be described as the study of relatedness, avoids the application of theoretical categories in order to understand the description of kin terms in their natural setting (Carsten, 2004). Emic approaches provide more elegant descriptions of linguistic categories: for example: amongst

the Maya Mopan, the term *tataa'* refers to father's elder brother and parent's father, but an emic description might be *male relative who is older than me and will provide care* (Danziger, 1993). As seen in the Maya Mopan example, emic descriptions often contain the prescription of behaviours or expectation (e.g. joking relationships, avoidance, or marriage).

Emic studies are much more flexible to the social complexity of kinship than etic approaches, providing insight to the lived experience of kin-based relationships within a society (Carsten, 2004). An etic approach can build a better understanding of how relationships between individuals are negotiated cross-culturally, and how individuals might navigate their social lives (Miller, 2007). In contemporary studies of kinship, using a standardised grid of relationships can often become a frustrating metric. Amongst many groups in Australia, kin relationships are applied to groups of people (called "skin" groups) who may not be tied to each other genealogically, rather than extending out from an individual, as how kinship is presented in English (McConvell, 2018). Similarly, families are constructed in increasingly diverse ways (particularly in western European countries), with single, and same-gender parent families, and new reproductive technologies increasing the variability of family construction (Stone, 2014). The emic approach of understanding kinship through experience provides a flexible analytical perspective which is adaptive to the unique microcosm of study, and helps us understand kinship at the individual, family, and sometimes community level.

The accurate representation of diversity (emic approach) and the search for legitimate cross-cultural patterns (etic approach) is an eternal tension within anthropology (D'Andrade, 2000). Emic, or social approaches, tend to be devoted to understanding the details of another person or people's world and offer a potentially unbounded view of human diversity. However, as we collate more information on human groups, patterns of similarity emerge demanding cross-cultural and evolutionary explanation (Gray & Watts, 2017). This thesis will apply macro-evolutionary ideas to examine the global diversity of kinship terminology and identify cross-culturally recurring structures. Where an emic approach focuses on understanding culture in the present, the focused outlook means long-term trends might never be uncovered. Using macro-evolutionary approaches alongside quantitative methods help to summarise the accumulation of data. The summaries help develop scientific and causal hypothesis for why we observe cross-cultural similarities. By identifying the cross-culturally recurring structures in kinship terminology, and the relationship of kinship terminology to social structure, we can inform our understanding of our kinship past, and how individuals and groups may have related to each other throughout our cultural history. It is the interest in human cultural history and global diversity that makes an etic approach more suitable to the goals of this thesis which are:

1. Assess the usefulness of existing kinship terminology typologies
2. Establish the global diversity of kinship terminology
3. Assess the relationship of kinship terminology to social structure and behaviour

Both etic and emic approaches have important applications within the study of kinship and kinship terminology, despite often being portrayed as opposing fields (Parkin, 2009). The etic, or genealogical approach used here is better suited for large-scale and quantitative comparative work because of the prototypical grid discussed above. However, it is important to be cautious of universal assumptions, in any broad scale analysis. When making generalisations about society for macro-analysis, there is some level of information that is necessarily thrown out. Quantitative approaches need always be aware of what is being thrown out, and how that variation may influence any conclusions.

A common critique of an etic approach when used to study kinship terminology, is an over-reliance on genealogical relationships for comparison (Schneider, 1984). This critique perhaps arose from a more general shift in anthropology during the 1970's, to a field of moral critique, and not of science (D'Andrade, 2000). But more specifically, there was a concern that the assumption of procreation as a central notion within the grid was unfounded (Shapiro, 2012). Over time, it became apparent that procreation and cultural understanding of kinship are important for different, but overlapping domains and after a period of reflection, the importance of genealogy to the comparative study of kinship terminology is beginning to find its place (Kronenfeld, 2012; Shapiro, 2012). Using a genealogical grid, research from corpus linguistics showed that genealogically close kin terms take longer to be replaced than kin terms for more distance relatives (Rácz, Passmore, Sheard, & Jordan, 2019, and Appendix E). Cognitive research use genealogically defined kinship terminology to show that simpler kinship systems are easier to learn (K. Smith, Frank, Rolando, Kirby, & Loy, 2020). Behavioural economics use a genealogical grid to show that both social and biological kin relationship guide cooperative behaviour (McNamara & Henrich, 2017). Amongst the Yanomamö (Venezuela / Brazil), a genealogical grid showed that cultural kinship ties were manipulated in order for men to maximise their potential spouses (Chagnon, 2017).

Next, I will define a number of important terms and abbreviations commonly used in the study of kinship terminology, which will help the discussion going forward.

1.1.2 Definitions

Here, I outline some definitions used within a genealogical approach to kinship. The first is the distinction between kin type, and kin term (Parkin, 1997). A kin type is used to describe a genealogical relationship, for example: father's father and mother's father are both kin types. A kin term is the word used to describe a kin type. In English, the kin term *grandfather* is used to described both the father's father and mother's father kin types, but in Djambarrpuyngu (Australia), there are separate terms for father's father (*maari*) and mother's father (*ngathi*). Kin types are the basis of the genealogical grid, and kin terms are the cultural categories that are laid on top of this grid (see figure 1.1).

Second is the term *ego*, which refers to the central figure of a kinship system, and the

person from which all relationship extend from. If it is not specified, the gender of ego is neutral and likely not relevant, however, there are cases where kin terms depend on the gender of the speaker. For example: In Māori, a man would refer to his elder brother as *tuakana*, and younger brother as *teina*, but a woman uses these terms for her elder sister, and younger sister respectively (figure 1.1). An emic interpretation of *tuakana* and *teina* might describe these words as *older* and *younger opposite-gender sibling*.

Thirdly, when graphically depicting a kinship terminology, as in figure 1.1 and figure 1.2, each shape represent a kin type. Circles represent women, triangles represent men, and squares indicate a gender neutral relative. Single lines between kin types indicate a genealogical relationship (or is a consanguine), and parallel lines indicate a marital relationship (or is an affine). The shape colour is used to indicate common kin terms between relatives, if shapes have the same colour, they use te same kin term.

Fourth, when referring to generations of relatives, I commonly use a shorthand indicated by *G* (for generation) plus a superscript indicating how many generations above (elder than) or below (younger than) ego are being discussed (see figure 1.2). Ego's generation is the centre of the terminology and is described as G^{0}. Ego's parent's generation is one generation above ego and described as G^{+1}, where the *+1* indicates one generation above. G^{-2}, indicates two generations below ego, or grandchildren, and so on.

I also use a common shorthand to refer to particular genealogical kin, to save describing the relationship in full sentences. In table 1.1, I give the basic description for each shorthand letter. The abbreviated relationship letters are concatenated to describe more distant and complex relationships. For example F is ego's father, FBD is father's brother's daughter, FBDeS is father's brother's daughters son who is elder than ego, mMeZD the mother's elder sister's daughter of a male speaker, and so on.

1.2 Kinship terminology and typology

Cognitive and social research shows that of all possible kinship terminology organisations there is a much smaller subset of plausible organisations (Kemp & Regier, 2012; Nerlove & Romney, 1967). The subset of plausible organisations occur because they obey the rules of cognitive efficiency, notions of genealogical distance, group membership, and social rank (Jones, 2010; Kemp & Regier, 2012). By studying the constraints on plausible diversity, it should be possible to identify the common structures of kinship terminology cross-culturally. From the constraints, and through understanding possible diversity, we can develop a typology of kinship terminologies that captures the breadth of diversity; ignores the noise arising from culturally specific deviations; and is predicted by patterns of internal (i.e. that a subsets of a terminology are predictive of other parts) and external co-selection (e.g. patterns of marriage or residence). To identify plausible diversity in kinship terminology, previous research starts with theoretically

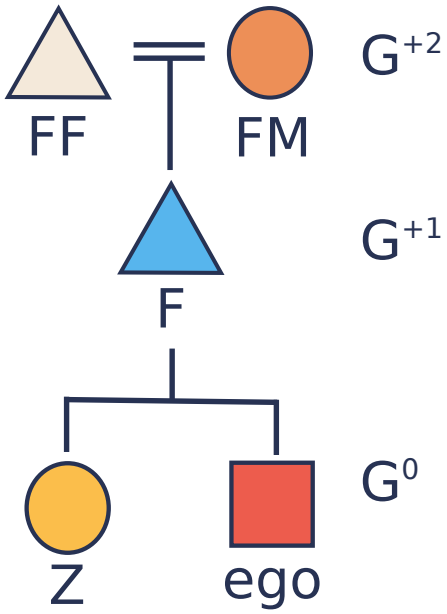

Figure 1.2: Letters underneath the shapes are coded descriptions of kin types. Codes can be aggregated to create more distant relationships, such as FF and FM here for father's father and father's mother. Letters on the right hand side highlight how generations are represented using notation. G^0 indicates all relatives in ego's generation. Moving to the generation containing ego's father is moving up a generation, and is therefore labelled G^{+1}. Moving up again is ego's grandparents generation, and is labelled G^{+2}. If we wanted to depict a generation below ego, this is moving down a generation and is labelled G^{-1}. As with figure 1.1, circles represent women, triangles represent men, lines represent genealogical relationships, and parallel lines indicate marriage.

Table 1.1: Shorthand kin type descriptions. As mentioned, G is also used to indicate generations. When G is used to describe generations it will always be followed by a superscript number, otherwise it is being used to describe a kin type.

Shorthand	Description
F	Father
M	Mother
P	Parent
B	Brother
Z	Sister
G	Sibling
S	Son
D	Daughter
W	Wife
H	Husband
e or y	elder or younger than ego
X or //	Opposite or same sex to ego
m or f	male or female speaker

possible diversity, constrained by cognitive efficiency, and reduces the possibilities to observed diversity, constrained by social organisation (Lowie, 1928; Nerlove & Romney, 1967).

Theoretical diversity is established by identifying all possible ways kin terms could be distributed for some set of relatives. For example: Nerlove and Romney (1967) found when analysing eight siblings kin types, there were 4,140 possible[2] organisations - but found 98% of observed diversity (n = 245) to be explained by only 12 types. The cognitive communicative principles of disjunctiveness, simplicity, and informativeness have been reliably shown to constrain the theoretical diversity of kinship terminology (Kemp & Regier, 2012). Because of a desire to reduce cognitive load, most theoretical organisations are unlikely to occur because they contain "disjunctive" categories or convey social information in sub-optimal ways (Greenberg, 1949; Kemp & Regier, 2012). A disjunctive category can be thought of as a category that groups the union of two attributes. For example: a category that contains all relatives who are male and all relatives who are elder than ego. A category based on these rules would contain a father's brother's son and an elder sister, but not a younger sister. In contrast, a conjunctive category is more akin to the intersection of attributes; *cousine* in French would be all relatives who are the child of a parent's sibling's and are female. The complexity and exceptional nature of disjunctive categories creates more cognitive load in contrast to the conceptually easier conjunctive category, making conjunctive categories more likely to occur (Bruner, 1986). Experimental evidence from two cultural contexts shows that disjunctive categories are harder to learn than conjunctive categories, leading researchers to assume kinship terminologies containing disjunctive categories are unlikely to occur, or are at least evolutionarily unstable (Ciborowski & Cole, 1972).

Having identified why much of the theoretical diversity does not occur, the obvious next step is to ask what structures observed diversity? Cognitive researchers have identified that kinship organisation needs to be optimised between simplicity and informativeness (Kemp & Regier, 2012). That is, there is a cognitive demand for a kinship terminology to be easy to learn and have as few words as possible (simplicity), but this trades off against the need to convey important social information (informativeness). The cognitive constraints of avoiding disjunctiveness, and trading off simplicity with informativeness, leave a much smaller subspace of plausible kinship terminology to choose from. Linguistic systems aim to be efficient, therefore have a drive to minimize cognitive load (or simplicity), but can only ever be as simple as the level of informativeness will allow (Kemp, Xu, & Regier, 2018). Since informativeness is constraining simplicity, the pressure to convey socially important information is likely to be driving cross-cultural diversity. Experimental evidence suggests that it is cultural norms, or informativeness, that drive cross-cultural variation in the observed subspace (K. Smith et al., 2020).

How social norms constrain observed diversity, and therefore how terminological diversity

[2]This is the 8^{th} Bells number. Bell numbers count the number of possible ways a set can be partitioned.

should be divided into typology is a point of continued debate, despite the cognitive constraints being relatively well understood (Kemp & Regier, 2012; Kemp et al., 2018). Existing research suggests observed diversity is related to differences in social structure, specifically: marriage, residence, descent, and inheritance practices (Jones, 2010; Murdock, 1949). However, empirically determining the relationship between the linguistic data of kinship terminology and behavioural data of social organisation has proved difficult. Quantitative challenges surround converting a list of words into a numeric structure amenable to statistical analysis, which historically have also been hindered by data availability and computational power (discussed further in chapter 3). If we already knew how variants of social structure aligned with changes in kinship terminology, then a typology would be straightforward to determine, however since this relationship is not obviously apparent, we must rely on alternative approaches. The approach most often used is to first divide kinship terminologies into types based on their similarities and differences, and analyse how these types align with social structure.

Typologies in general are useful analytical tools for exploring cross-cultural similarities and developing causal models of variation. By summarising a domain into a set of discrete categories, a typology will emphasise theoretically interesting aspects of a variable domain, and exclude the noise and variability in the data which might mask important trends. However, typologies only achieve these goals under the important condition that they accurately describe the divisions in diversity observed in the world (Kronenfeld, 2006). Kinship has often been a focus for typological work because of the constraints on diversity and the suggestion of probabilistic, if not deterministic, links between kinship terminology and external selectors of social organisation, and strong patterns of internal coherence (Godelier, 2012; Murdock, 1949). Revealing these links would unlock an important window into the behaviour of our ancestors through linguistic reconstruction of kinship terminology, as well as understanding a part of the complex intersection between culture and biology. However, kinship terminology diversity is yet to be categorised in a way that satisfactorily reveals these relationships.

Existing typologies of kinship terminology derive from the combinatorial possibilities of a finite set of rules, such as *difference of generations*, or *gender of the relative named* (Kroeber, 1909; Trautmann, 2001). The most commonly used typology contains six organisations, which I refer to throughout the thesis as the **six-piece typology**. This typology contains six main types, namely: *Eskimo-type*, *Hawaiian-type*, *Dravidian-Type*, *Sudanese-type*, *Crow-type*, and *Omaha-type* (see box 1.1 for more details on these types). This typology is theoretically derived by combining two rules: *Difference between lineal kin and collateral kin kin* (or collaterality) and *the gender of the person through whom the relationship is traced* (or the rule of bifurcation), and the principle of generational skewing (applying kin terms across generations) (Godelier, 2012; Kroeber, 1909). A theoretically derived typology identifies a set of rules from the ethnographic record, then combinatorially applies these rules to create a typology from the top, down. Theories of external and internal co-selection were developed from this typology, to

fit with the exemplary structure (e.g. cross-cousin marriage leads to the linguistic distinction of cross-cousins; Goody, 1970). But many of these relationships were not empirically derived and were often left untested, or were supported using unsatisfactory statistical approaches (e.g. Murdock, 1949, ; and in chapter 2).

The theoretically derived six-piece typology has often grated against the inconvenient truths of observed kinship terminology organisation (Parkin, 1997). For example: this typology does not distinguish between the types of crossness found in Iroquois-types, and those found in Dravidian-types (Trautmann & Barnes, 1998). Within the relationships the six-piece typology is concerned, Dravidian and Iroquois types are structured identically, but Iroquois-types have a separate system for affinal relatives (relatives defined through marriage), where Dravidian does not (see box 1.1 for more detail). Likewise, it does not differentiate between Hawaiian-systems that distinguish siblings and cousins by gender, and those which distinguish be relative gender (chapter 5, section 5.6.2). As time drew on, anthropologists often found exceptions to the types, or argued for the creation of sub-types, suggesting the descriptive and predictive qualities of this typology was not meeting the needs of working anthropologists. From a macro and cross-cultural perspective, and as this thesis will lay out, this typology also lacks any external (chapter 2) and internal (Passmore et al., In preparation) predictive power. This is most explicitly tested in chapter 2, where I test 18 existing anthropological co-evolutionary theories regarding kinship terminology and cultural practices across 176 societies. However, many theorists believe a typology that is both descriptive and predictive to be possible, which is the goal of chapter 5 (Allen, 2009; Godelier, 2012; Lounsbury, 1964).

In general, theoretical approaches to typology, while based on some ethnographic information, often fail to appreciate the breadth of observed kinship terminology diversity at the global scale. Without appreciating diversity it is not possible to fully understand the constraints that might cause cross-cultural differences (Evans, 2010). All typologies hide variation by design in order to minimise noise and emphasise the patterns of variation which are theoretically interesting (Kronenfeld, 2006). However, within the study of kinship terminology, as more ethnographic information has become available, and more terminologies were collated (e.g. chapter 3), the variation this typology captured and described is no longer considered sufficient for modern anthropological theory.

When typologies, like the six-piece kinship terminology typology, are used widely this also means the variation described by the typology is over-emphasised and variation that is omitted is under-explored. In kinship terminology, this has led to unattested generalisations, for example: the six-piece typology generalises to a single pattern of cross kin (categorisation of parent's opposite-gender siblings), whereas research has identified different patterns of crossness which create opposing predictions in relation to social structure - I discuss this more below (Godelier, Trautmann, & Tjon Sie Fat, 1998; McConvell & Hendery, 2017). Equally, typologies under-explore diversity that is not captured by the by the categories within the typology. For

example: distinctions such as relative age or relative gender are globally common, but do not feature in kinship typologies - meaning we have little understanding of why these distinctions persist cross-culturally and what their function is. The misrepresentation of kinship terminology diversity through typology has hindered theoretical progression in the study of kinship organisation.

While many practising anthropologists, working in emic and cross-cultural domains recognise the shortcomings of the traditional typologies, they are convenient categories for other social scientists. Sometimes the typology is used as the basis for new theories, but more often it is used as proxies for behavioural patterns in correlational studies. For example: evolutionary psychologists have used the six-piece typology and the tenuous link to behavioural patterns (Guillon & Mace, 2016, and chapter 2) to propose hypotheses of fitness interdependence (Cronk et al., 2018), where as economists have used the six-piece typology to infer the likelihood of cousin marriage when data was missing (Enke, 2018; Schulz et al., 2019).

Nevertheless, the anthropological and linguistic literature has recorded a recurrence of kinship terminology structures across geographically distance and historically unrelated societies, as will be described in chapters 4 and chapter 5. The regularity in linguistic kinship structures across the globe suggest there are some, if not universal, statistical regularities in how kin are organised. To do the intriguing patterns of human cultural variation justice, and move forward in explaining as well as describing them, it is important that we provide a typology that captures the right level of variation.

Box 1.1: Murdock's six-piece typology

Hawaiian

The theoretical Hawaiian kinship system terminologically divides kin by generation and gender. This results in four terms which can be represented by the following rules:

$$F = FB = MB$$
$$M = FZ = MZ$$
$$B = FBS = MBS = FZS = MZS$$
$$Z = FBD = MBD = FZD = MZD$$

These rules could be more elegantly described as the cultural kin-categories of a male in the generation above, a female in the generation above, a male in my generation, or a female in my generation. The syncretisms across parent's siblings (male and female) in G^{+1} are often echoed by syncretisms in the descending generation between siblings and parents' siblings' children. That is, if all G^{+1} women are terminologically equivalent, then

the syncretism should be reflected in their children. Traditional expositions of kinship typologies notwithstanding, it is important to emphasise that organisation in G^{+1} does not cause the organisation in G^0, but merely that there is a process of co-selection in terms of a natural fit between terminological systems in the two generations.

Eskimo

Eskimo terminologies distinguish "lineal family" members (up and down the direct line of descent), from "collateral kin" (off to the side of this direct line), and collapse kin terms for collateral kin (e.g. the two types of uncles [FB, MB] and aunts [FZ, MZ]). This typically results in seven or eight kin terms describing G^0 and G^{+1}. These terms are structured by the following rules:

$$F \neq FB = MB$$
$$M \neq FZ = MZ$$
$$B \neq MZS = MBS = FZS = FBS$$
$$Z \neq MZD = MBD = FZD = FBD$$

These rules distinguish nuclear family members from other relatives, and ignore lineal distinctions in parent's siblings and their children. This system is often linked to the cultural importance of nuclear families, although evidence suggests considerable variance in the social organisation of societies using this system (Hughes, 1958). In a similar vein to Hawaiian systems, there are predictable equivalences between G^{+1} and the descending generation. These equivalences are exemplified by English: aunt's and uncle's give birth to cousins, but parent's give birth to sons or daughters. This projects a natural harmony between the G^{+1} and G^0 generations, since the lineal vs collateral distinction in the parents' generation is propagated into a similar distinction (between siblings and cousins) in ego's generation.

Iroquois / Dravidian

Iroquois and Dravidian systems are distinguished from the previous two types by introducing "crossness". This is where parent's opposite- (or cross-) gender siblings are terminologically different to their same-gender (parallel-) siblings (Kryukov, 1998). The distinction between same- and opposite-gender siblings is generally thought to co-select for a similar cross-gender pattern in the descending generation. A canonical Iroquois or Dravidian system is described with the following rules:

$$F = FB \neq MB$$
$$M = MZ \neq FZ$$
$$B = FBS = MZS \neq FZS = MBS$$
$$Z = FBD = MZD \neq FZD = MBD$$

Within these equations, Iroquois and Dravidian are identical. However, Dravidian systems have no separate system for affinal relationships, where Iroquois does (Désveaux & Selz, 1998). The lack of seperate affinal terms in Dravidian systems is attributed to a direct link with cross-cousin marriage, meaning many affinal relatives are also consanguineal relatives. For example: when marrying your father's sister's daughter, your father's sister also becomes your mother-in-law.

Sudanese

A canonical Sudanese system distinguishes all three structural positions in the parents' generation (i.e. siblings on each side have their own term), and the cousin terms track these distinctions. Such systems eliminate all syncretisms relevant to the major typologies.

$$F \neq FB \neq MB$$
$$M \neq MZ \neq FZ$$
$$B \neq FBS \neq MZS \neq FZS \neq MBS$$
$$Z \neq FBD \neq MZD \neq FZD \neq MBD$$

Murdock, within his Ethnographic survey, distinguished between Sudanese and Descriptive types, which are structurally the same but differ in whether the terms are internally analysable (Murdock, 1967). Danish, for example, would be considered a descriptive type in the parents' generation, since FB is *farbror* (*far* "father", *bror* "brother"), MB is *morbror* (mor "mother"), and FZ and MZ are the only slightly less transparent faster and *moster* (combining fa < far and mo < mor with -ster < *søster* "sister").

Omaha / Crow

Unlike the previous four systems, which are defined by syncretisms (or lack of syncretisms) within generations, Omaha and Crow systems are defined by their syncretisms

across generations, often called generational skewing. These systems are effectively mirror opposites, where Omaha systems skew along patrilineages, and Crow systems skew along matrilineages. This is highlighted in the second rule for Omaha, and the first rule for Crow below; the "skewing" syncretisms are shown in bold.

Omaha	**Crow**
$F = FB \neq \mathbf{MB} = \mathbf{MBS}$	$F = \mathbf{FB} = \mathbf{FZS} \neq MB$
$M = \mathbf{MZ} = \mathbf{MBD} \neq FZ$	$M = MZ \neq \mathbf{FZ} = \mathbf{FZD}$
$B = MZS = FBS \neq FZS$	$B = FBS = MZS \neq MBS$
$Z = MZD = FBD \neq FZD$	$Z = FBD = MZD \neq MBD$

The nature of skewing in each of these systems has been imputed to societies with strong patrilineal and matrilineal descent, respectively. For example, in the Omaha system, both one's MB and one's MBS are "male members of one's mother's patriclan". The skewing illustrated here is restricted to G^0 and G^{+1} and these rules represent a typical Omaha or Crow system, though there are languages which propagate the skewing right down the generations of a matriline or patriline.

1.2.1 Modern failings of a historic typology

The six-piece typology, described in box 1.1, is the most widely used kinship terminology typology, and is often used as the primary description of a languages kinship terminology (Dole, 1972; Murdock, 1949). Designed to capture the linguistic classification of cousin organisation, it also aligned with an existing G^{+1} typology (Lowie, 1928). Each type was named after a society that exemplified the system: *Eskimo-type*, *Hawaiian-type*, *Dravidian-Type*, *Sudanese-type*, *Crow-* and *Omaha-type*. As described in the previous section, these types were derived from two rules: the rule of collaterality and the rule of bifurcation, which create the terminology for the first four types in the above list across ego's generation (G^0) and ego's parent's generation (G^{+1}) (Godelier, 2012). The application of generational skewing then creates the *Omaha-type* and *Crow-type*.

To understand why this typology is so widely used, it is important to consider the interests of anthropologists preceding the development of the six-piece typology. By understanding the academic interests, it helps us understand why certain decisions were made and what the goals of the typology were. Shades of the six-piece typology began to appear in the late 19^{th} and early 20^{th} century (Lowie, 1928; Morgan, 1871). During this time, anthropology, and science in general, was on the search for universal characteristics of society, with the aim of understanding how society moved from "primitive promiscuity" to "modern Euroamerican

monogamy" (Trautmann, 2001). A Eurocentric theoretical focus arose to fill a gap of knowledge brought about by the "time revolution". That is, prior to the *Origin of Species*, the story of human origin was discussed within the bounds of Latin or biblical chronology (Darwin, 1859; Trautmann, 2001). Evolutionary theory, as it was proposed by Darwin, caused a revolution in the scale of human history, and demanded an explanation. Much of the research coming out of the time revolution had an inexcusable penchant for European superiority, and therefore, often looked to develop theories resulting in a trajectory of evolution towards European ideals (e.g. Morgan, 1851, 1871). The racist desire for a uni-lineal and directed theory of evolution required simplicity and sometimes erroneous depiction of society.

Early "evolutionary" models of kinship terminology change highlight the simple and erroneous depictions of society. For example: kinship in Hawaii was considered the most "primitive" form of kinship, and laid the basis for the origin of kinship by Morgan's account (Gardner, 2008). The kinship terminology used in Hawaii was (unsurprisingly) a Hawaiian-type (box 1.1), which co-lexifies wife and wife's sisters, as well as husbands and husband's brothers (Gardner, 2008; Morgan, 1871). This co-lexification was reasoned to represent recurrent promiscuity between adults, and frequent brother-sister marriage (Handy & Pukui, 2012; Morgan, 1871). Morgan reasoned that the lack of linguistic distinction created "confusion" amongst the locals for who they were related to and who they were not, hence promiscuous and incestuous relationships were permissible. The centrality of Hawaiian-kinship to Morgan's theory meant that despite no evidence of cohabiting siblings, these facts were assumed to ensure continuity in the grandiose explanation of societal progression, placing sexuality at the center of societal development (Gardner, 2008). But, the claims of promiscuity amongst the Hawaiians were established upon erroneous linguistic grounds - where the relationship was more likely to represent extended family ties, rather than sexual promiscuity (Gardner, 2008; Handy & Pukui, 2012).

The six-piece typology as we know it today, arose out of the collation of data collected within the book *Social Structure* (Murdock, 1949). From the mid-20$^{\text{th}}$ century the typology began to gain traction, although also drew many critics. Those who endorsed the typology derived numerous theories about how the structure of each type was encouraged by various external forces, such as marriage or descent (Goody, 1970). Critics however, bemoaned the inflexibility of the typology to variation, particularly in capturing Australian kinship terminology diversity (Lévi-Strauss, 1969). The tradeoff between simplicity and inflexibility characterises much of the debate surrounding the typology up to the modern day (Kronenfeld, 2006). The simplicity of the typology makes it a useful pedagogical tool, and the centrality of kinship to daily life makes the six-piece typology an engaging introduction to cultural diversity (e.g. Stone, 2014). However, researchers who aim to explain the origins of society demanded a more descriptive typology, which reflected a more general move in anthropology to the appreciation of diversity (Hannerz, 2010). The shift in academic interests to capturing more diversity to explain human societal origins has seen Murdock's six-piece typology become unfavourable amongst kinship

specialists, critiqued for both theoretical and pragmatic failings.

Theoretical critics highlight that the rules used to create the six-piece typology mix structural (e.g. lineal vs collateral relatives) and genealogical (e.g. how cousins and siblings are categorised) properties (Read, 2013). By building typologies on a mix of frameworks (structural rules vs genealogical relatedness) there is no single theoretical foundation from which to build on. Others have critiqued the typology's inability to sufficiently incorporate structural differences - famously not identifying the different crossing rules between Iroquoian and Dravidian style organisation, and the inflexibility to capture divergent types, such as Aluridja kinship[3] (Godelier, 2012; Romney & Epling, 1958). Social anthropologists have argued the typology overemphasises the etic understanding of kinship and ignores the emic meaning of kinship terms. That is, while languages might be structurally identical, the kinship terms between these two languages may still hold different meaning and reflect different social organisations (Kronenfeld, 2006).

To take a contemporary anthropological perspective: in order to understand the cross-cultural similarities in human societies, it is important to understand the breadth of observed diversity (Evans & Levinson, 2009; Hannerz, 2010). The study of *observed* diversity (over theories on possible diversity) reflects the collation of data, the advancement of statistics, and a desire to test many of the existing theories on the structure of human diversity (Ember & Levinson, 1991). As with any scientific endeavour, not every theory will be right, no matter how beautiful or harmonious, and the testing of theories against diversity is the most expedient way to figure out which theories have substance. Within the field of kinship, an exploration of diversity has led to the division of existing types (see Tjon Sie Fat (2018) for variants of crossness or Kronenfeld (2004) for general discussion), alongside calls to redevelop the long-standing categorisations of kinship terminologies (Kronenfeld, 2006). The interest in diversity is reflected in the development of generative approaches to terminology description, which I discuss next (Jones, 2010; Read, 2013). The usefulness of the six-piece typology as a pedagogical tool means breaking the grip of this characterisation will be difficult. This thesis will focus on how we can best capture kinship terminological diversity for theoretical advancement.

1.2.2 Recent theoretical approaches

Recently, theoretical approaches to kinship terminology have sought to develop generative methods to understand how any particular terminology is constructed, using Optimality Theory (OT) (Jones, 2010) and algebraic approaches (Read, 2013), rather than developing new typologies. Generative approaches create a flexible framework from which the observed diversity can be reconstructed. The shift to generative frameworks highlight a desire to accurately

[3]Without going into too much detail when Alrudija systems were discovered they broke a number of perceived rules in the relationship between kinship terminology and behaviour. For example: Aluridja appeared to allow marriage between classificatory siblings, but this actually works within a complex system of generational moieties (Godelier, 2012)

represent diversity, but also a shift to understanding the mechanisms creating such diversity. Both OT and the algebraic approaches use a small set of rules (or equations) that interact to generate the organisation of a particular language's kinship organisation, or subset of. I give a brief overview of these approaches, before suggesting how generative models of kinship terminologies may provide the tools we need to develop flexible and predictive typologies.

OT is a general theoretical approach, used in other branches of linguistics (particularly phonology) to understand structural properties of language (Smolensky & Prince, 1993). A more detailed description of this theory, and its application to kinship terminology, can be found in two papers by Jones (2003a, 2003b), but I give a brief overview here. First, the process requires an input, which in the case of kinship terminologies would be a set of kin types. An example set might be: father, father's brother, and mother's brother (for simplicity I ignore relative age). The input is passed to the generative stage where all possible combinations of kin types are created. There are five possible ways to categorise our example set: a single term for all three relatives, a term for each relative, and three possible ways of having two terms for the three relatives (e.g. English uses *father* for father and *uncle* for mother's and father's brother). The generated possibilities are then filtered through a set of ordered rules (or constraints) specific to a language, until only one candidate remains, which becomes the optimal output. Every language has the same rules, but variation in the order creates diversity. The order is determined by the information people need to convey, which is in turn likely driven by social norms, aligning with cognitive constraints of informativeness and simplicity (Kemp & Regier, 2012; Levinson, 2012). Rules are also violable and ordered in terms of importance, allowing for asymmetrical organisation. The order of the rules varies by language, which gives rise to cross-linguistic diversity. In chapter 4, I also predict that rank order of rules influences the likelihood that a particular rule would change (i.e. higher ranked rules are less likely to change than lower ranked rules). As discussed by Jones (2003b), it is unlikely that any individual goes through this process each time they need to determine the label for a particular kin member - nor as they are learning kinship terminologies, which is likely to occur via memorisation. But OT might provide explanations for the diversity in kinship terminology over evolutionary time, using rule order to identify variation in organisation and likely patterns of change.

The algebraic approach, on the other hand, is designed specifically to understand kinship organisation, and attempts to integrate both the genealogical kinship grid with an emic understanding of relationships (for a detailed description see Read (2013) or Read et al. (1984)). The approach divides kinship terminologies into two key components, the objects (which are kin terms) and operations (the equations that determine kin terms). These are combined in algebraic equations which describe a terminology. A particular language is divided into three levels of analysis; kin-term structure (independent of genealogical structure), kin terms as mapped onto genealogical structure, and finally the sets of rules applied to kin terms. This approach argues for the separate analysis of genealogical and kin term organisation in order to incorporate

both the local understanding of kinship organisation that overlays the genealogical structure dictated by biology. This is unlike the application of OT to kinship, which is only concerned with the categorical structure of terminologies.

Both of these approaches provide generative models for describing linguistic organisation in a particular language, but their power lies in the ability to quantify cross-linguistic diversity by providing a new form of prototypical referent. Focusing on OT: since each language is theoretically described by a finite set of rules, where variation is generated from rule order, comparing the order of rules between any pair of languages should be indicative of their similarity.

The key difference between the generative and genealogical prototypical referent is the unit of analysis. For genealogical approaches it is the kin type, and generative approaches it is the rule or equation. From an evolutionary perspective, the unit of selection is what is evolving: do we believe the cultural grouping of kin types drives terminological change, or are categories derived from the intersection of higher level rules? Genealogical approaches are more primitive, in that the level of data they produce is at a more granular level, but, generative approaches potentially reflect how terminology is psychologically constructed (Jones, 2003a). In chapter 4 and chapter 5, I attempt to draw the benefits of both these approaches, but ultimately rely on the kin type as the unit of evolution.

1.3 Summary

As interdisciplinary research is increasingly interested in using kinship organisation to understand social change (Schulz et al., 2019), cooperation (McNamara & Henrich, 2017), and language evolution (Lansing et al., 2017), there is now a demand for kinship theorists to offer consensus on the structure and divisions of kinship terminology diversity. With an analytically defined typology, kinship theorists can a) understand the uncertainty in the data they rely on and b) can be comfortable with other domain's relying on the typologies that are presented.

The rest of this thesis continues as follows: chapter 2 provides statistical test on the evolutionary patterns found in the existing six-piece typology. This chapter uses evolutionary models to quantitatively assess ancestral kinship organisation, likely paths of transition, and co-evolutionary relationships with aspects of social structure - finding little evidence of universal rules. The conclusion from this analysis is that there is a need to reassess the existing kinship terminology typology through understanding the extent of kinship terminology diversity. To do this, I introduce Kinbank, a database of 1,151 kinship terminologies from across the globe in chapter 3. This database collates data at the level of kin type, providing a lower level of granularity from which to test cross-cultural hypotheses. In chapter 4, I set out a morphospatial approach to understand kinship terminology diversity, and in chapter 5 I set out to quantitatively estimate that diversity. Chapter 4 looks to establish the limits of kinship terminology diversity based on current theoretical and ethnographic literature. Conceptualising

these ideas in a morphospatial domain, which I name kinspace, allows us to understand the highly-dimensional domain of kinship terminology diversity. In chapter 5, I use dimensionality reduction techniques to approximate the space that is conceptualised in chapter 4. This computational approach to kinspace explores the structural regularity in kinship terminology within the Kinbank database. This chapter emphasises the recurring structures found in existing literature occur in our new database, but that that within-type diversity is considerably higher than most theoretical approaches might assume. Chapter 6 explores how kin terms interact with behaviour. By comparing behavioural responses in two languages with differing kinship terminology, I begin to explore how kinship terms coordinate behaviour.

Finally, I offer some concluding remarks on kinship terminology and the importance of diversity, and how the need to understand diversity is important when building typology, but also more generally when attempting to understand the complexity of the human condition.

Additionally in Appendices E, F, and G, I attach three other papers that I contributed to during the course of my PhD. Appendix E is a corpus linguistic approach to understanding kinship term evolution. Using a sample of 47 languages from Indo-European, my co-authors and I show that kinship terms that are used frequently are replaced at a slower rate than less frequently used terms. Importantly, frequently used kinship terms are replaced less often than basic vocabulary words, but more often than basic vocabulary words when used infrequently. We propose that this reflects the non-independence of kinship words which create a system, and since the sample is only Indo-European, highlights the modular nature of kinship terminology when reflecting social structure. In this case, reflecting the importance of the nuclear family in our sample of languages. I contributed by performing the automated cognate-detection, and phylogenetic modelling, and contributing to the writing of the final paper.

Appendix F is a complexity approach to kinship terminology typology. Here, we tested the relationship of kinship terminology typology to social structure and to measures of social complexity (such as population size). Using a global sample of 936 societies from the Ethnographic Atlas (K. R. Kirby et al., 2016; Murdock, 1967), we found that kinship terminology typology had no relationships to population size, but was predicted by patterns of marriage and descent, as well as shared ancestry. This result highlights that kinship terminology reflects the cultural norms of society, coordinating expectations of behaviour, rather than being a reflection of the size of any particular community. I contributed the phylogenetic modelling to this paper.

Appendix G deviates from the kinship theme of this thesis, but applies the core message of maximising diversity into the domain of religious world-view. This paper uses text-analytics to understand the variation between religious and non-religious individuals in their understanding of the world. By using text-analytics, we do not need to restrict participant response to likert scales, but can allow them to express themselves in a more natural format. Here, I aided in the conceptualisation, data curation, analysis, and writing of the paper.

CHAPTER 2

No universals in the cultural evolution of kinship terminology

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2.1 Kinship terminology and typology

All human societies recognise categories of kin with language that specifies how people are related. These categories are expressed linguistically in kinship terminology, a system of words for relatives. Globally, the patterning of these category systems is variable, yet displays widespread typological convergence. Together with community norms of behaviour towards kin, kinship terminologies are fundamental aspects of human social diversity (Murdock, 1949). Over time, kinship organisation structures both cultural (Buckley & Boudot, 2017) and genetic (Lansing et al., 2017) diversity, so understanding the drivers of change in this domain provides insights into cultural evolution more generally. Despite the potential for unbridled variation, kinship terminologies are remarkably constrained. The universe of terminological systems for labelling siblings, cousins, parents, and parent's siblings is 10,480,142,147 theoretically possible[1] varieties (Nerlove & Romney, 1967). Yet historically, cross-cultural diversity in kinship terminology has been considered sufficiently represented by only a handful of major types, for example, the six-piece typology of cousin-organisation by Murdock (Murdock, 1949, figure 2.1).

[1]This is the result of the 16th Bell number

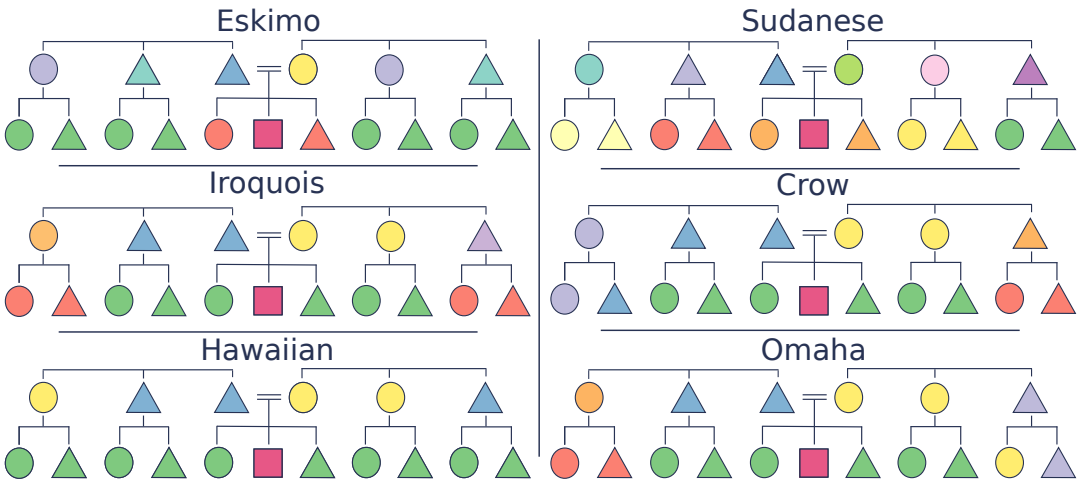


Figure 2.1: Six terminological types as formalised by Murdock, and named after societies in which they were first identified (Murdock, 1949). Triangles represent male, and circles female, relatives. The square represents ego, the focal point of the terminology. Relatives are coloured to indicate where the same linguistic label (word) is used. Parallel lines indicate marriage.

2.1.1 Constraints on diversity

Recent research shows that kinship terminologies may optimise between minimising cognitive load (simplicity) and reliably communicating intended meaning (informativeness) (Kemp & Regier, 2012). These constraints may account for limits on observed variation, but do not explain why we observe any variation at all, nor the origin and maintenance of particular variants. Experiments have demonstrated a cognitive bias for simplicity in kinship terminology and language-learning more generally, which explains the absence of many theoretical possibilities. Simplicity is limited by the need to communicate social information, meaning informativeness limits simplicity and drives cross-cultural variation. Since informativeness is conveying social information, it is likely shaped by local cultural practices (S. Kirby, Tamariz, Cornish, & Smith, 2015; K. Smith et al., 2020).

Anthropologists routinely propose that kinship categorisation is shaped by organisation of social structure, specifically, kinds of inheritance, descent, marriage, and residence (Jones, 2010; Murdock, 1949). If norms of social structure act as global drivers of informativeness for kinship organisation, they also provide causal (although not necessarily deterministic) hypotheses of change about kinship terminologies (see table 2.1 and table S3). Broadly speaking, social norms act to transmit cultural beliefs on (e.g.) sex, respect, obligation, and the spatial proximity of kin, all of which affect and are affected by how kin are categorised. For example, nuclear family organisation might mean relatives outside this unit live at a distance, reducing the frequency of interactions and therefore the need to linguistically distinguish amongst types of relatives such as cousins, as in Eskimo-types and typical of English (Murdock, 1949, figure 2.1). Hypotheses of this sort stem both from the accumulation of ethnographic observations or

deductive reasoning, and are supported in the literature with simple cross-tabulations (Goody, 1970; Murdock, 1949). However, these hypotheses were derived using outmoded statistical tools and no longer represent the current state of kinship theory. It is increasingly clear that shared ancestry plays a significant role in explaining patterns of cultural diversity, not least in the domain of kinship (Guglielmino, Viganotti, Hewlett, & Cavalli-Sforza, 1995; Mace & Jordan, 2011). Much anthropological "common-knowledge" concerning kinship is therefore subject to the problem of phylogenetic auto-correlation, where societies are related by common descent. Each society does not represent an independent occurrence of a phenomenon, thus violating assumptions of statistical independence (Naroll, 1965). Here I address these issues by using phylogenetic comparative methods (PCMs) to explore the cultural evolutionary patterns of kinship terminology diversity, particularly testing so-called drivers of change. This is not the first application of phylogenetic methods to kinship organisation; these approaches have been successfully applied within language families to understand ancestral states and feature-based patterns of change (Jordan, 2011). However, in this paper I present the first cross-language-family phylogenetic analysis of the drivers of kinship terminology.

2.1.2 Quantitatively reviewing kinship terminology typology

Kinship terminology theory has developed as a speciality field away from the broad typological distinctions developed in the early 18th century, but Murdock's ideas are consistently revived in the broader anthropological sphere (Cronk et al., 2018; Guillon & Mace, 2016; Stone, 2014). While recent theorists have debated the biological underpinnings of kinship distinctions (Chapais, 2009); have explained terminology diversity by invoking constraint rules and optimality theory (Jones, 2010); and developed new approaches of kinship algebra (Read et al., 1984), the standard typology persists. Here, I intend to systematically review the usefulness of this typology as a descriptive and predictive tool through systematic hypothesis testing using modern comparative methods. Our quantitative macro-evolutionary approach can contribute new insights to existing debates, arbitrate long-standing assertions with new methods, and offer insight to under explored areas of kinship diversity (Gray, Greenhill, & Ross, 2007).

To progress our understanding of kinship terminology evolution, I use language phylogenies in combination with ethnographic sources of cultural data to infer ancestral states of kinship terminology, to estimate patterns of evolutionary change, and to test for correlated evolution with aspects of social structure. Bayesian posterior samples of phylogenies mitigate and specify uncertainty about both the branching histories of populations, as well as the evolutionary model of cultural change. I use data from D-PLACE and the ethnographic atlas (d-place.org, K. R. Kirby et al., 2016; Murdock, 1967) for kinship terminologies and social structure in three large language families (Austronesian, Bantu and Uto-Aztecan), totalling 176 societies (Gray, Drummond, & Greenhill, 2009; Grollemund et al., 2015; Levinson, Greenhill, Gray, & Dunn, 2011). These three families have different time depths and environmental histories, allowing us

to probe universality in the patterns of change.

2.2 Materials and Methods

2.2.1 Data and phylogenies

I selected Austronesian, Bantu, and Uto-Aztecan language families because of their large size, and cultural data availability. These languages families cover 14% of the societies in D-PLACE, and 20% of the phylogenetic diversity, giving different evolutionary time depths (Austronesian = 5.5ka; Bantu = 4ka; Uto-Aztecan = 5ka), geographic environments and ecological pressures. Cultural data was paired with the most recent published linguistic phylogenies for Austronesian (Gray et al., 2009), Bantu (Grollemund et al., 2015), and Uto-Aztecan (Levinson et al., 2011). Posterior samples of 1000 phylogenies were used in all cases. All terminological and social data was taken from the Ethnographic atlas subset of D-PLACE (K. R. Kirby et al., 2016; Murdock, 1949, dplace.org). Any societies with missing data were pruned. Co-evolutionary methods required binary data: see Appendix A table S2 for coding decisions for data availability in each hypothesis. Longitude and latitude for each society were also taken from D-PLACE. Hypotheses were found through exploration of the literature and using the "Explaining Human culture" database (Ember, 2018).

2.2.2 Phylogenetic signal tests

I performed five tests to assess whether shared ancestry was a constraint on kinship diversity. The phylogenetic "D" test uses simulation to determine whether the clustering of binary variables on a phylogeny follow patterns of Brownian motion (D = 0 indicates perfectly Brownian clusters, D < 0 strong clade clustering) or random clustering (D = 1 indicates complete randomness) (Fritz & Purvis, 2010). Mantel tests assessed the importance of geographic signal. Mantel tests use random permutation and Pearson's correlation statistics to determine the correlation between two matrices. I compared log geographic distance, calculated with the Haversine formula, to a binary similarity matrix of each terminology present in each language family, for 999 permutations. Phylogenetic distance was calculated using cophenetic distance, and the cophenetic function in base R (Team, 2018). To determine whether phylogenetic or geographic distances best determined the distribution of terminologies, I used partial Mantel tests controlling for either geographic or phylogenetic distance while testing the other against kinship terminology similarity.

2.2.3 Ancestral state inference

I estimated the probability of a particular terminology at the root of each language phylogeny and estimated the patterns of change between each state. I then performed Bayesian reversible-

jump Markov Chain Monte Carlo (MCMC) ancestral reconstructions of kinship terminologies for each language family using BayesTraits V 3.0 Multistate (Pagel & Meade, 2017). Multistate uses a posterior of phylogenies to estimate the probability of each terminology present in the taxa at the phylogeny root, and an estimation of the rate (Q) matrix. The reversible-jump approach searches the model space for an optimal solution by dynamically setting some rate parameters to zero. The Q matrix shows the likelihood of changing from any state to any other. MCMC chains were run for 10^9 iterations, sampling every 50,000 iterations with a burn-in of 10,000 iterations, resulting in a posterior of 19,999 iterations. A stepping stone sampler was used to estimate the marginal likelihood. For all trees I used an exponential prior (λ=10). I used 100 stones sampled every 1000 iterations. Each analysis was run three times to ensure MCMC convergence, and was tested using the Gelman-Rubin diagnostic (Gelman & Rubin, 1992). Due to uncertainty in the reconstruction of the Bantu ancestral state, each possible taxon was fossilised as the root to estimate likelihoods. I calculated pairwise log Bayes Factors (BF) to assess the evidence for each response. Fossilised ancestral state reconstruction was used on the Bantu language family in an attempt to parse the most likely ancestral state. I forced the model to assume an ancestral state and used model comparison to determine the evidence for each possible ancestral state.

2.2.4 Co-evolutionary tests

Co-evolutionary tests were performed by comparing dependent and independent phylogenetic Bayesian reversible-jump (RJ)-MCMC models of evolution using BayesTraits V3.0 Discrete (Pagel & Meade, 2017). See Appendix A for the number of iterations, burn-in length, sampling rate, and priors for each analysis. Each analysis ran three times to ensure consistent MCMC convergence and used Gelman-Rubin diagnostics. The posterior from the first sample is presented in the results. To determine whether a dependent or independent model better fits the data, I use log Bayes Factors.

2.3 Results and Discussion

2.3.1 Ancestral states

Tests for phylogenetic signal (vertical transmission) and spatial auto-correlation (horizontal transmission) demonstrate that the diversity of kinship terminologies in all language families is structured by shared ancestry, and justifies the use of PCMs (Appendix A, table S4). In Austronesian and Uto-Aztecan, shared ancestry was the clear driver of diversity. The separation of vertical and horizontal transmission was less clear in Bantu, suggesting multiple processes may be acting in this language family.

Ancestral state inference of kinship terminology in each language family shows strong support for an Eskimo-type terminology at the root of the Austronesian language family

(Pr(*Eskimo*) = 0.847; 89% High density interval (HDI): [0.58, 1.00]). In Bantu there is weak support for an Iroquoian-type root (Pr(*Iroquoian*) = 0.395; HDI: [0.13, 0.67]). I "fossilise" the ancestral kinship state for Bantu and find weak evidence for an Iroquoian-type root over the next most likely state, Hawaiian-type (BF = 2.31) and all other possibilities, using the likelihood model comparison metric log Bayes Factors (BF) (Appendix A table S11). In Uto-Aztecan, there is no outright support for any terminology, the most likely being Hawaiian-type (Pr(*Hawaiian*) = 0.311; HDI: [0.23, 0.49]). Fossilising ancestral states did not provide any additional evidence. Details on model convergence diagnostics and baseline probabilities are available in Appendix A.

In Austronesian languages, ancestral state results can inform the debate on kinship in Proto-Malayo-Polynesian (PMP), an early ancestral speech community c. 4kya. The "bilateral hypothesis" suggests that the ancestral state of PMP was Hawaiian-type, because many contemporary societies in the geographical south-east Asian home of PMP exhibit social structures that align with this kinship organisation, such as cousin incest taboos, limited polygyny, and sexual equality (Murdock, 1949). The alternative "symmetric-exchange hypothesis" suggests that ritualized marital exchange structured PMP society, rather than the features listed above (Lévi-Strauss, 1969; Wouden, 1968). Under the assumption of symmetric exchange, linguists reconstructed the PMP terminology to an Iroquoian-type (Blust et al., 1980). Using phylogenetic inference, Eskimo-type was deemed the most likely ancestral state (Pr(*Eskimo*) = 0.897).

Both the bilateral and systematic exchange hypotheses rely on certain assumptions. First, both hypotheses use comparative ethnography, which accords preference to societies that are geographically close to family "homelands" in inferring ancestral social structure. In contrast, PCMs use information from all societies in the family and let us explore a wider range of models of how social norms change. Second, kinship typology are assumed to to have deterministic links to social structure. Using PCMs, I show in section 2.3.3 that the relationship between terminologies and social structure is weak at best.

In Bantu, previous phylogenetic reconstructions using the same data sources for kinship terminologies find evidence of Hawaiian-type terminologies as the most likely ancestral state, with some support for an Iroquoian-type (Guillon & Mace, 2016). In this study I use a newer phylogenetic posterior tree sample that contains more languages (see Appendix A, section "Guillon and Mace comparison"). However, for both Guillon and Mace (2016) and my Bantu reconstructions, the likelihood of any particular terminology being ancestral is considerably lower than in Austronesian. This could be evidence of borrowing between Bantu societies, also supported by signal tests (Appendix A, table S4), or it could reflect the relatively limited contemporary diversity in Bantu (i.e. the preponderance of Iroquoian-type). Borrowing may have occurred between Bantu societies, and/or with other non-Bantu sub-Saharan languages: we do not have methods to incorporate the latter in ancestral state inference. However, for example by analogy, genetic and linguistic evidence shows Khoe-Sān women married into South-Western

Bantu societies, following the patrilocal tradition commonly found in this region (Pakendorf et al., 2017). Other papers have recorded systematic language borrowing throughout the Bantu family (Barbieri et al., 2014; Holden & Gray, 2006; Oliver, 1982). The uncertainty seen in the Bantu ancestral state inference suggests a multitude of cultural evolutionary processes (beyond stochastic change) are at work. Previous Bantu research suggested that shared ancestry is the pervading macro-evolutionary process through which kinship norms are transmitted (Guglielmino et al., 1995; Mulder, George-Cramer, Eshleman, & Ortolani, 2001). We know that many interdependencies are likely to drive cultural evolution (at minimum, shared ancestry and borrowing), but these results highlight that their relative impact varies across language families.

Phylogenetic reconstruction is useful in regions where there has been less comparative research, such as Uto-Aztecan. Traditional linguistic reconstructions of Proto-Uto-Aztecan terms suggests a terminology system unlike any of the six common types, with a Hawaiian-style organisation in the generation of ego, but unique terms for each member of the parental generation (G^{+1}), consistent with a Sudanese-type (Shimkin, 1941). The Uto-Aztecan reconstruction finds Hawaiian-type cousin terms most likely, possibly reflecting the ego-generation-focused (G^{0}) classification of kin terminologies used in our analyses, but this cannot be interpret with confidence. The six-piece typology is technically agnostic with respect to G^{+1}, but much writing on kinship assumes internal consistency between G^{0} to G^{+1} (Cronk et al., 2018; Godelier, 2012). A drawback of phylogenetic modelling is that it only infers ancestral states that exist as observed states: the linguistic reconstruction of Proto-Uto-Aztecan as Sudanese-styled G^{+1} is compatible with the analyses because parental-generation variation is not captured in the data used. This demonstrates two wider points: that internal variation exists within any existing kinship type (not all terminologies are "pure"), and that little systematic data on the global structure of that variation is available, including how societies transition between types (Murdock, 1949). In this particular case the phylogenetic and linguistic reconstructions of Uto-Aztecan terminology suggests that kinship organisation may change in a more modular way than is currently being assumed, and modelled with these data.

The ancestral state analyses infer different basal terminologies (starting states) in each language family. It also shows us that while there is evidence of phylogenetic inheritance in the distribution of kinship terminologies, the lack of confidence in ancestral states suggests a second, non-inheritance process also acting on kinship organisation. I now briefly explore the potential for transitions between kinship terminology to follow some universal or generalising pattern, as seen in other semantic domains such as the evolution of colour terms (Berlin & Kay, 1991; Haynie & Bowern, 2016).

2.3.2 Transitions in typology

Ancestral state inference can estimate the direction and rate of change from one terminological type to another (a transition, figure 2.2). This information can be used across language families to conclude whether kinship terminologies follow consistent patterns of change, or whether change is lineage-specific. Since there are 36 transitions to estimate (a multi-directional transition between each of the six states) I use RJ-MCMC methods, meaning negligible transitions are constrained to zero. Constraining negligible transitions to zero avoids over parameterising the model. Statistically important transitions are determined via the posterior-to-prior odds following Currie, Greenhill, Gray, Hasegawa, and Mace (2010). I calculate the prior likelihood of a single transition rate model and compare this to the number of times a particular transition is estimated in the posterior. Posterior-to-prior odds of less than 1 suggest that parameter is unlikely to be equivalent to zero. Here I discuss all transitions with posterior-to-prior odds less than one in each language family. The odds of all transitions are shown in Appendix A, tables S14-16. This is a very broad approach to analysing transitions, in that I only explore relatively extreme changes (from one organisation to another), and do not allow transitional types to exist. Previous work has explored patterns of evolutionary change using a feature based approach, which offers a more detailed understanding of how kinship organisation changes over time (Jordan, 2011). Unfortunately, this data is not available in the cross-cultural setting used here, but the typology-level analysis should reveal high-level patterns of change, and whether we can observe any similar patterns of change between language families.

All statistically important transitions are shown in figure 2.2. In Austronesian, there are important shifts from Crow-type to Hawaiian-type (posterior-prior odds = 0.349), Eskimo-type to Hawaiian-type (0.386), and Hawaiian-type to Iroquois-type (0.461). In Bantu, the only important shift observed is from Iroquois-type to Omaha-type (0.420), with the next most likely transition being from Iroquois-type to Hawaiian-type (1.053), followed by Omaha-type to Descriptive-type (1.182). In Uto-Aztecan, six important transitions were identified: the first three are transitions to Hawaiian-type from Iroquois-type (0.123), Crow-type (0.371), and Eskimo-type (0.459). The second three are all transitions to Iroquois-type from Hawaiian-type (0.585), Eskimo-type (0.907), and Crow-type (0.922).

There is one shared sub-graph between Austronesian and Uto-Aztecan: Crow-type and Eskimo-type transition to Hawaiian-type, and Hawaiian-type transitions to Iroquois-type (the red arrows in figure 2.2). The shared sub-trajectory presents a potential bottom-up model for future research to pursue. Compared to existing models of change, there is support for transitions from Crow-type to Hawaiian-type (generational), but support for the opposite direction in the remaining transitions: Eskimo-type to Hawaiian-type, and Hawaiian-type to Iroquois-type (Kryukov, 1998).

A long standing debate within terminology transitions is whether they are uni- or multi-directional (Trautmann & Whitely, 2012). This is a complex question, some theorists have

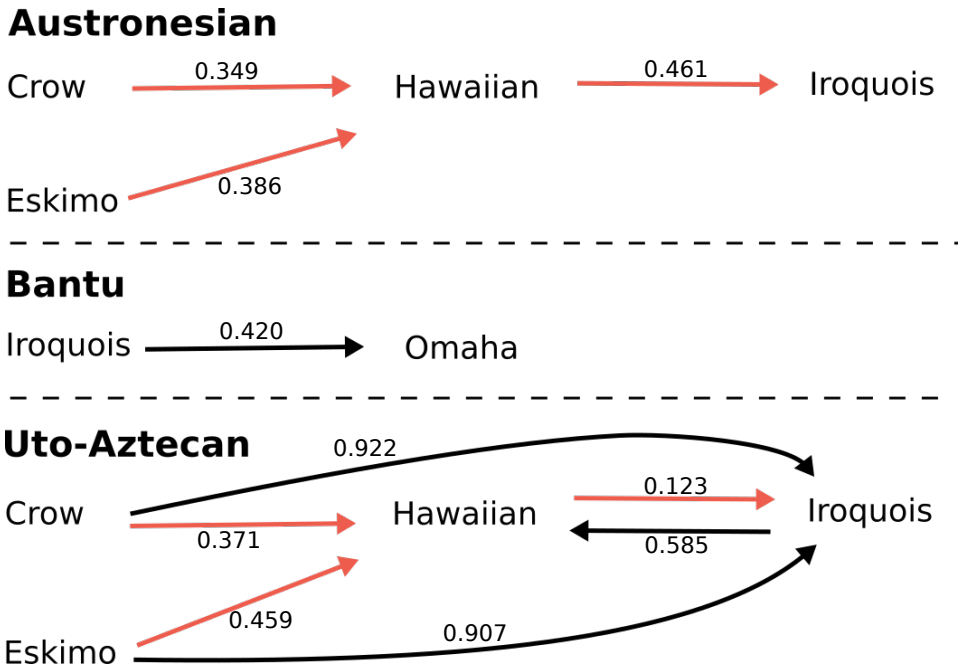


Figure 2.2: Transitions with posterior-prior odds for each language family. Red lines indicate repeated sub-graphs.

argued strongly for a unidirectional pattern (Allen, 1989; Kryukov, 1998), however more recent research is undecided (Trautmann & Whitely, 2012). The evidence from the model shows most change is unidirectional, but there is some evidence of multi-directional change in Uto-Aztecan. Combining these pieces of evidence suggests that a multi-direction pattern of change is a more likely trajectory for kinship terminologies and is reflective of the adaptive relationship of kinship terminologies to local cultural, economic, and ecological conditions.

If kinship terminologies were primarily linguistic outcomes of a cognitive communicative pressure for simplicity, our ancestral state and transition models could be expected to show more generalised patterns of change across all language families. The results in this paper only observe similarities between a maximum of two languages families, and non-identical patterns between these two. The recurrence of the sub-graph could be understood as evidence of universal patterns of change, but I would emphasise the importance of additional transition in Uto-Aztecan. While in Austronesian the sub-graph implies a unilineal trajectory, Uto-Aztecan models of change are much more flexible and highlight a unique and much more complicated model of evolution. A common perspective is that kinship terminologies are a "social-semantic product" of complex and potentially locally-specific adaptive pressures such as demography and resource control. The differences between language families may be the result of these more local differences. I test this perspective by examining the most common broad-scale explanatory drivers of kinship terminology diversity, that terminology are social-category responses to forms of social organisation

2.3.3 Tests of Co-evolution

I identified 18 theories within the anthropological literature which suggest kinship terminologies are determined by patterns of social organisation: marriage, descent, and residence (Murdock, 1949). When operationalised against available data, they total 29 separate statistical hypotheses of the correlates of kinship terminologies (table 2.1 & Appendix A table S3). Bayesian phylogenetic models of co-evolution allowed me to test the evolutionary relationship between social structure and kinship terminologies, while controlling for patterns of shared ancestry. I ran models of dependent and independent evolution and determined which model best fits the data using log Bayes factors (BF). A BF greater than ten indicates strong support for a dependent model of evolution, greater than three positive support and less than three no support (Kass & Raftery, 1995). To assess universality, hypotheses are tested in each family (Austronesian, Bantu, and Uto-Aztecan) as data allows, giving a total of 57 tests. I find some support for 14 of the 18 theories, but only 19 of the 29 statistical hypotheses. Only two theories are supported across two language families - none in all three. Only 19 of 57 tests were supported overall, emphasising the lineage specific results of kinship terminological diversity.

2.3.3.1 Marriage

These hypotheses include allowable or preferred cross-cousin marriage and the acceptance and rate of polygyny. If cross-cousin marriage is prescribed, a linguistic signal discerns marriageable and unmarriageable cousins, as in Iroquoian-types (Goody, 1970). There was positive evidence that Iroquoian-types co-evolve with the allowable and preferred cousin marriage (BF = 9.14 and BF = 9.79) in Austronesian, and strong evidence that they co-evolve with a preference for cousin marriage in Bantu (BF = 13.85). Despite the prevalence of this theory in historical literature, recent scholars do not believe Iroquois-type is compatible with cross-cousin marriage (Lounsbury, 1964). Instead, it is the alternative Dravidian-type which is considered to fit with patterns of cross-cousin marriage (Trautmann & Barnes, 1998). This result suggests a need for investigation within Austronesian Iroquoian-type societies to determine whether they offer counter-evidence for this theory or languages have been misclassified. I explored the relationship between cross-cousin marriage and Iroquois-types in Bantu further, and found a particularly stable relationship between Iroquoian-types and preferential cross-cousin marriage that can be traced back to an early clades; but is not present in the most early-branching societies in the group. Ancestral node 70 showed a high probability of both an Iroquoian-type organisation and a preference of cross-cousin marriage (P(Iroquoian and cross-cousin marriage) = 0.77, see figure 2.3), which was inherited in 56% of descendant societies. Ancestral node 70 temporally aligns with the Bantu expansion through the Savannah corridor 4kya, around modern Gabon and Republic of Congo (Grollemund et al., 2015). The Savannah corridor hypotheses proposes that climate change caused Savannah habitats to encroach on the rainforest, guiding Bantu migration. It is plausible that the combination of environmental change and increased migration

resulted in demographic change, influencing social structure and changing kinship organisation. Future research may be able to utilise models of maintenance in order to properly explore this proposal (Ross, Strimling, Ericksen, Lindenfors, & Mulder, 2016). In contrast however, Uto-Aztecan societies in my sample with Iroquoian-type organisation never practice cross-cousin marriage, highlighting the lineage-specific processes apparent within the ancestral state analysis. It is also proposed that the prohibition of cousin marriage leads to the terminological conflation of all cousins, or cousins and siblings, as seen in Eskimo- and Hawaiian-types (Goody, 1970). There was positive evidence of Hawaiian-type co-evolving with no preference for cousin marriage (BF = 5.42), however in line with previous evidence, there was no link between the prohibition of cross-cousin marriage and Hawaiian-type or Eskimo-type cousin organisation (Dole, 1972).

Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel kin cousins, which prevents merging of lineal kinship terms (Murdock, 1949). This results in terminologies with different terms for parent's opposite sex siblings, as found in Iroquois- and Crow-types. There was weak support that Iroquoian types evolved with high rates of polygyny in Austronesian (BF = 2.53), but not low levels of polygyny. There was positive support for Eskimo-types co-evolving with monogamous marriage in Austronesian (BF = 7.36).

2.3.3.2 Residence

Recent phylogenetic models have shown residence patterns to evolve in lineage specific ways (Moravec et al., 2018). Changes in residence patterns may shift kinship terminologies, because residence affects proximity and interaction with kin (Chapais, 2009). Avunculocal (living with a maternal uncle), patrilocal (living with or near the husband's family), and matrilocal residence (living with or near the wife's family) bring together lineal relatives in the parental generation (G^{+1}) and are thought to result in terminologies which collapse parental terms with their same-sex siblings (e.g. father and father's brother). These are collectively described as unilocal residence, which are thought to correlate with Iroquois-, Crow-, or Omaha-types (Murdock, 1949). Here, the types are analysed collectively (as unilocal residence), and independently (as avuncu-, patri-, and matrilocal residence). In Austronesian, there was strong support for avunculocal residence co-evolving with Crow-types (BF = 10.37), positive evidence for unilocal residence co-evolving with Crow-types (BF = 4.23), and positive evidence of unilocal residence co-evolving with Iroquois-types (BF = 6.44). In Bantu, there was positive evidence between Iroquois-types and matri-avunculocal residence (BF = 4.46), but no relationship between other patterns of unilocal residence and terminological types. Previous work has explored the relationship between Iroquois-types and unilocal residence in Bantu, and also found no relationship (Guillon & Mace, 2016). In Uto-Aztecan there was strong support for a relationship between Iroquois-types and unilocal residence (BF = 5.29). There was positive support for co-evolution

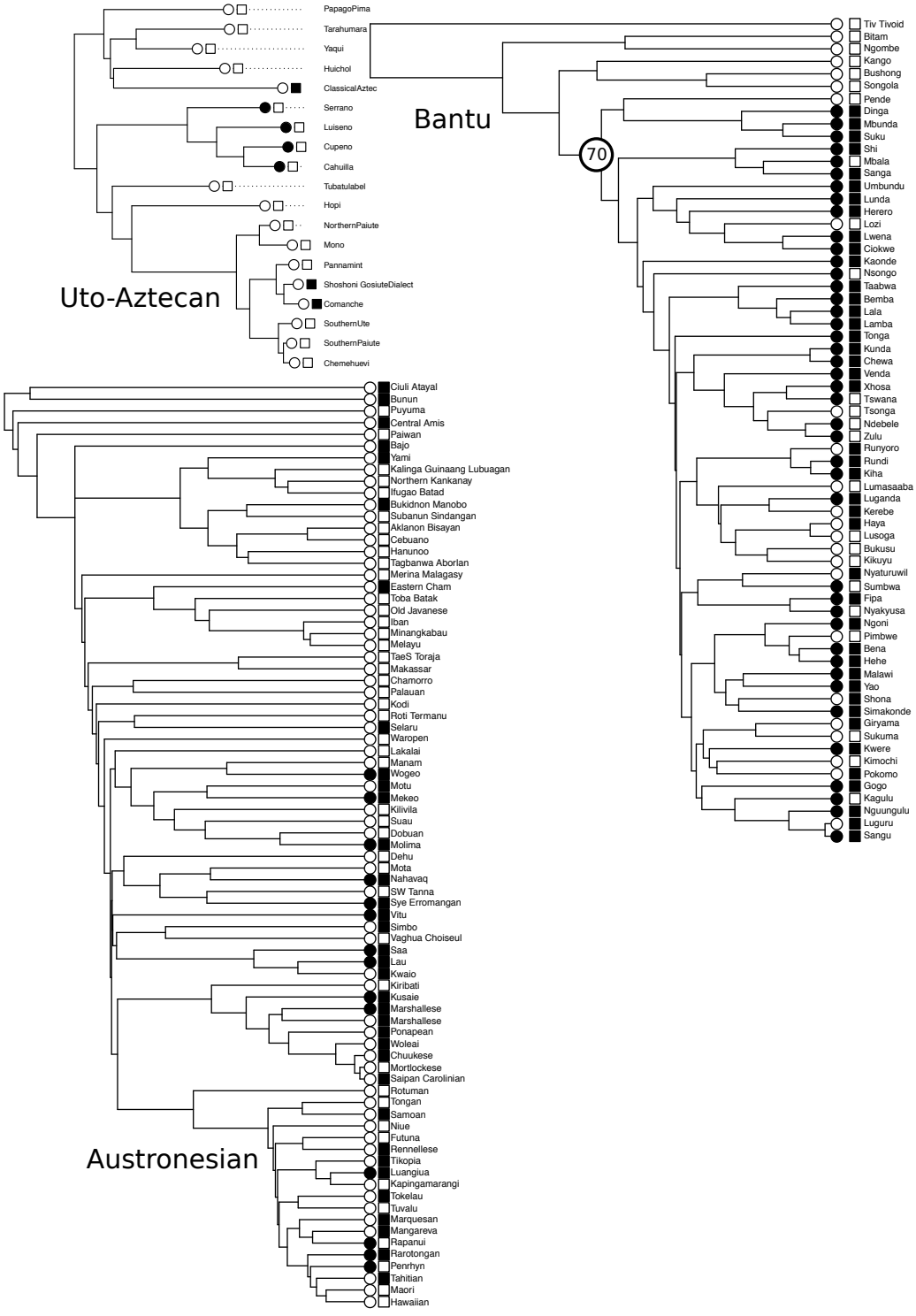


Figure 2.3: Indicative co-evolutionary relationship between Iroquois terminologies (circles) and preferential cross cousin marriage (squares). Black indicates the presence of a trait, white indicates absence. Dotted lines indicate non-contemporary societies. There is strong support for this relationship in Austronesian (BF = 9.79), and Bantu (BF = 13.85), but not in Uto-Aztecan. I also explored the dual inheritance of these traits in Bantu from node 70. All trees are maximum clade credibility trees.

between patrilocality and Omaha-types (BF = 6.42) in Bantu in contrast to previous analysis (Guillon & Mace, 2016), and between matrilocality and Crow-types (BF = 3.41), in Austronesian. However, when virilocality and uxorilocality are included under patri- and matrilocality respectively, there was only positive evidence for matrilocality in Austronesian (BF = 2.5). Bilocal residence is thought to have the opposite effect to unilocality, bringing some collateral and some lineal relatives together through both sexes. This combination of relatives overrides the distinctions between groups and collapses terms into Hawaiian-type terminologies (Murdock, 1968). However, there is no support for Hawaiian-types and bilocal residence co-evolving, confirming previous phylogenetic results found in Bantu (Guillon & Mace, 2016). I extended this hypothesis to only include societies that reside with extended family groups but still found no support. Eskimo-types linguistically separate and emphasise the nuclear family, which is also perpetuated through neolocal residence. There is positive support for the relationship between Eskimo-types and neolocal residence (BF = 7.98), but not the cultural importance of nuclear families.

2.3.3.3 Descent

Social groups may align themselves based on common ancestry or descent, which increases the importance of specific kin-relations (also known as social differentials; Chagnon & Irons, 1979). Unilineal descent patterns prioritise one family line (paternal or maternal) over the other (Murdock, 1949). There was positive support for Iroquois-types and unilineal descent in Austronesian and Uto-Aztecan (BF = 7.10 and BF = 9.71). Where possible, data was constrained to societies that also practised exogamy, reflecting a prediction from Murdock but found no support for this restricted test (Murdock, 1949). As with residence, the importance of distinguishing patri- and matrilineal relatives was supported: by a strong relationship in Austronesian with Crow-types and matrilineal descent (BF = 10.45), and positive evidence (BF = 3.34) of Bantu Omaha-types co-evolving with patrilineal descent (Goody, 1970), in contrast to Guillon and Mace (2016) previous work. Bilineal societies do not promote the social differential of either lineage, and so is often associated with Hawaiian-types, which there was strong evidence for in Austronesian (BF = 10.70) (Murdock, 1970).

Overall, only some of the previously theorised social norms co-evolved with kinship terminology, and this was largely specific to a single language family. Many relationships are not supported when accounting for shared ancestry. It is possible that some unsupported relationships are "phylogenetically inert" stable pairings of terminology and social structure, but I estimate this is only likely in three of 57 tests (see Appendix A, table S84). I examined marriage, descent, and residence as classic drivers, however, recent research has shown links between structural social change and religion (Watts et al., 2016), and land-tenure (Sheehan, Watts, Gray, & Atkinson, 2018), these moderating factors could influence kinship organisational change and be tested in future.

Table 2.1: All tests of co-evolution between terminologies and social structure. Each row indicates a statistical hypothesis, and columns indicate the language family in which the test is performed, with cells containing log Bayes Factors. BF <2 indicates weak evidence, >2 positive evidence, 5-10 strong evidence, and >10 very strong evidence. Figures in bold show results with log Bayes Factors two and above. Where there was no data available to test the hypotheses, the cell is left blank. See table S3 for the source and quote for each hypothesis.

Hypothesis	***AN***	***BT***	***UA***
Crow & Polygyny (high rates)	1.059		
Crow & Matri-avunculocal residence	**10.374**	-1.536	
Crow & Matrilineal descent	**10.45**	-1.82	
Crow & Matrilocal residence	**3.401**	0.753	
Crow & Polygyny	-1.839		
Crow & Uni-local residence	**4.228**	-2.231	
Eskimo & an absence of permitted cousin marriage	-0.323		
Eskimo & an absence of preferential cousin marriage	-2.423		
Eskimo & Bi-lineal descent	-1.634		
Eskimo & Monogamy	**7.368**		
Eskimo & Neo-local residence	**7.984**		
Eskimo & Nuclear families	0.963		
Hawaiian & an absence of permitted cousin marriage	0.211	-2.07	-1.114
Hawaiian & an absence of preferential cousin marriage	**5.421**	-2.77	-1.632
Hawaiian & Bi-lineal descent	**10.7**	-1.44	-1.567
Hawaiian & Bi-local extended family	0.945	-1.756	-0.298
Hawaiian & Bi-local residence	-1.547	-2.097	-0.171
Iroquois & permitted cross-cousin marriage	**9.135**	0.132	-1.607
Iroquois & preferential cross-cousin marriage	**9.785**	**13.85**	-1.189
Iroquois & Exogamy with uni-lineal descent	0.205	-2.012	-1.319
Iroquois & Polygyny (high rates)	**2.528**		1.854
Iroquois & Matri-avunculocal residence	-3.243	**4.458**	-1.269
Iroquois Polygyny	-1.425		
Iroquois & Uni-lineal descent	**7.101**	-1.586	**9.705**
Iroquois & Uni-local residence	**6.441**	-2.486	**5.29**
Omaha & Matri-avunculocal residence		0.232	
Omaha & Patrilineal descent		**3.336**	
Omaha & Patrilocal residence		**6.424**	
Omaha & Uni-local residence		-2.09	

I am confident these results accurately model the available data, but do not conclude that earlier anthropological work was mistaken in postulating social norms as drivers of terminological change. Instead, I suggest these results reflect the explanatory limits of the existing typologies. This paper highlights the inadequacies of the Murdock typology as a tool used to infer behavioural organisations, but I emphasise its inability to accurately describe global variation. For example, Lozi (Western Zambia) and Tongan (Polynesia) have kinship terminologies

which are both classified as Hawaiian-type. Lozi distinguish cousins based on their sex, while Tongans distinguish cousins based on the sex relative to the speaker. Using more granular data we could explore the structure of the typological variation, identify subtle but important differences in kinship types across language families, or identify paths of evolution that result in convergent terminological types.

2.4 Conclusion

I have analysed kinship typology across three language families of different time-depths and environments and have been unable to discover strong universal drivers or unidirectional patterns of evolution in kinship terminology types. Partially, this is attributed to the insufficiency of the typology in representing global kinship terminological diversity at the right level of detail. For ancestral state reconstruction and transitions, the typology offers a restrictive view of change. It fails to incorporate within-type variation, or between-type variation by only allowing transitions between attested fixed states. The co-evolutionary results may similarly be considered as the result of insufficient specification by the Murdock typology. However, I note that in the literature underlying the set of hypotheses tested here, scholars proposed or observed these associations using this typology: it may be a clumsy categorical tool, but it was the framework within which these anthropological relationships were largely proposed. More constructively, it is possible that many of the social-semantic relationships that I tested were not supported because the kinship terminologies contain sub-types, "hidden" through categorisation in Murdock's scheme. For example, the disentanglement of Iroquoian-type and Dravidian-types identified key linguistic differences that made opposite predictions concerning cross-cousin marriage (discussed above; Trautmann & Barnes, 1998).

The academic utility of this typology may have reached its limits. Future research to explore the existence of sub-types or variants will require comprehensive lexical data. In chapter 3, I discuss the "Kinbank" database, a collection of kinship terminologies from a global sample. Fine-grained complete terminological data can be coded to represent key social and linguistic distinctions, allowing us to more realistically characterise types and patterns of change by focusing on the reconstruction and transitions of features (such as age or gender, see Jordan (2011)).

The key message here is that universal relationships linking kinship terminology and social structure are not supported. This is not because one or two societies do not follow a trend: for most of the hypotheses tested, we could not conservatively even claim "statistical regularity". Cross-cultural universals have come under increased scrutiny as improved data are more readily available (K. R. Kirby et al., 2016) and phylogenetic methods are adapted for cultural questions. For example, similar methodological studies show lineage specific processes of word-order evolution across Indo-European, Austronesian, Bantu, and Uto-Aztecan (Dunn,

Greenhill, Levinson, & Gray, 2011), and lineage-specific transitions in post-marital residence in the above language families plus Pama-Nyungan (Moravec et al., 2018). These results clear the ground for more detailed characterisations of kinship organisation in future.

Chapter 3

Kinbank: A global database of kinship terminology

This chapter is adapted from a paper that I am preparing for submission to Nature Resources. I wrote and performed analysis for all sections, with the exception of section 3.4, where the analysis was performed by Wolfgang Barth, and written by me. Due to the collaborative nature of this project, this chapter has received commentary from my collaborators, but is primarily my own authorship.

Co-authors who contributed to the manuscript are: Fiona Jordan, Nicholas D Evans, Simon J Greenhill, Catherine Sheard, Wolfgang Barth, and Kyla Quinn.

Co-authors who contributed to the data collection are: Joshua Birchall, Luis Henrique Oliveira, Jasmine Calladine, Maisie Ford, Paraskevi Argyriou, Isobel Clifton, Angarika Deb, Lucy Harries, Jo Hickey-Hall, Péter Rácz, Seán Roberts, Ewan Thomas-Colquhoun, Anouk Diederen, Lieke Hoenselaar, and Maarten van den Heuvel.

3.1 The usefulness of kinship terminology to Anthropologists

Human kinship organisation is remarkably diverse. Our mating, social, and cooperative relations with kin show more variation than any other species on the planet, despite kinship being anchored in biological and social constraints (Jones, 2010). Kinship relations and family ties are created in human communities not only through basic reproductive processes but are also created by social processes in the transmission of language and culture (Chapais, 2014). Because kinship is so central to social organisation it influences many aspects of our evolutionary history: the distribution of language and genetics (Lansing et al., 2017), technology (de la Croix, Doepke, & Mokyr, 2018), as well as the likelihood of external warfare (Divale, 1974).

Understanding diversity in kinship is therefore important in understanding human migration, cultural evolution, and linguistic change.

The study of kinship by anthropologists has traditionally encompassed marriage forms and customs, the tracing of descent and community relations, the jurisdiction of rights and responsibilities in offspring and the variety of residential groupings for family (e.g. Murdock, 1949). In the last half-century, this remit has broadened to include the study of new reproductive technologies, single-parent and same-gender parent families, and LGBT+ kinship (Stone, 2014). While research foci change, one consistent core strand of study has been the linguistic denotation and organisation of family members in kinship terminology: the patterned vocabulary of words for kin. Kinship terminology can be viewed as a complex phenotypic expression of the genealogical relations of kinship (Chapais, 2009), the cognitive constraints of linguistic efficiency (Kemp & Regier, 2012), and the cultural variability of social organisation (Jones, 2010). This chapter introduces Kinbank, a database of kinship terminology which centralises and systematises cross-cultural data on kinship terminology; connects to existing cross-cultural databases; and links terminology to phylogenetic trees; with the goal of facilitating the understanding of kinship, and kinship terminology diversity.

3.2 The need for centralisation

Kinship terminology has a deep history in anthropology and linguistics (Morgan, 1871); indeed, virtually all ethnographic and descriptive linguistic scholars in the 20^{th} century elicited kin terms from speakers in the communities they studied. As a result, kinship terminology is well-documented in the anthropological and linguistic literature. Kinship terminology data has been collected through some comparatives surveys (Murdock, 1949), they are often documented within ethnographies (Malinowski, 1922), and sometimes are contained in word lists (Ekstrom, 1959). While each collection contains its own organisation, there is a lack of over-arching systematicity tying the documentation together. By centralising and systematising the literature in an open and digital format, Kinbank provides a resource that can quantitatively estimate the cross-cultural diversity of kinship terminology; test existing hypotheses on the relationship between language and social structure; and revive interest in an omnipresent cross-cultural domain as an open access and transparent resource.

There have been some previous attempts to collate literature on kinship terminology, but many collections remain in personal (Bancel, de l'Etang, & Bengtson, 2015) or paper-based (Morgan, 1851; Murdock, 1949) databases, making them impractical for modern collaborative work. Contemporary anthropological databases are freely accessible, transparently constructed, and most often digital (K. R. Kirby et al., 2016; Watts et al., 2015). An example of a detailed regional survey of kinship terminology is Austkin (Dousset, Hendery, Bowern, Koch, & McConvell, 2010). Austkin shows the power of centralised and systematised kinship terminology

through its transparency and desire for collaboration, while preserving kinship terminologies for Australian Aboriginal languages. The Austkin project has uncovered new knowledge on Pama-Nyungan Proto-kinship terms (Hendery & McConvell, 2013), patterns of borrowing (Koch, 2013), and patterns of change (McConvell, 2013), offering a trajectory this database hopes to emulate on the global scale.

Anthropology, psychology, and linguistics have all recently taken a (re)turn to kinship terminology. Cognitive models of kinship organisation highlight strategies to uncover universal processing principles (Kemp & Regier, 2012); social categories of kinship are seen to influence pairwise cooperation (McNamara & Henrich, 2017); differences in marriage, descent and residence patterns are though to drive cross-cultural variation in several psychological dimensions (Schulz et al., 2019); cross-cultural research demonstrates the strong links between linguistic and social organisation (Rácz, Passmore, & Jordan, 2019, and Appendix E); corpus-based studies have shown the difference in evolutionary change between kinship words and basic vocabulary (Rácz, Passmore, Sheard, & Jordan, 2019, and Appendix F), and several studies have shown how kinship can even find its way into core grammar (Blythe, 2013; Evans, 2003). Systematically organised data sources of kinship terminology will be central in further multidisciplinary research, allowing us to understand the purpose of cross-cultural variability in kin categorisation across evolutionary, social, and linguistic domains.

While some kinship terminology is known widely (e.g. Iroquois-type, Hawaiian-type, etc.), the extent of global diversity is rarely discussed outside specialists within anthropology (e.g. Godelier et al., 1998), and as such we know little about the implications of variation in kinship terminology. Sometimes, minor categorical divergence in terminology can have significant implications on the compatibility with external predictors. For example: Iroquois- and Dravidian-type terminology are identical when comparing G^0 and G^{+1}, but Iroquois systems have a separate set of terms for relationships define through marriage (affinal relationships), where Dravidian does not (Lounsbury, 1964). The lack of terms for affinal kin in Dravidian is attributed to a relationship with mandatory cross-cousin marriage, meaning genealogical relatives and affinal kin are often the same person. That is, marrying a cross-cousin means a relative is both a spouse and parent's opposite-gendered siblings child, a father's sister can also be a mother-in-law, and so on. The examination of minor differences within terminology, and how they reflect broader social differences have long needed further exploration, but currently within-type variation is ignored in favour of high-level grouping (Godelier, 2012; Murdock, 1949).

Here I present Kinbank, a collation of kinship terminologies from 1,151 languages across the world. This database aims to encourage the interdisciplinary and transparent analysis of a truly cross-cultural domain that is central to human cultural diversity. First, I discuss data collection, sampling procedures and the structure of the database; I then briefly discuss data reliability. Two example analyses follow. The first example shows the depth of the database by

examining the phonological structure of "nursery words" (mother and father terms) in a global sample of 1,022 languages. The second analysis highlights the promise of Kinbank in testing cultural hypotheses using anthropological databases and language phylogenies, by examining the relationship between cross-cousin marriage and bifurcate-merging terminology in a sample of Bantu languages.

3.3 Data, sampling, and database structure

Kinbank provides a digitised, open-access, and global database of kinship terminologies, resulting from the collaboration of two aligned research projects: Parabank at the Australian National University, and VariKin at the University of Bristol. The database is freely accessible at https://doi.org/10.5281/zenodo.4020442.

3.3.0.1 The etic approach

As discussed in section 1.1.1, there have been two approaches to kinship terminology: emic (language-internal logic) and etic (objective language-independent grid for comparison) (Evans, 2010). The constructivist, or emic approach, seeks to unlock the inner logic of a languages kinship terms by taking locally meaningful categories of terms as a fundamental unit of interest. For example: the Kayardild (Australia) kinship terms *kularrint* and *duujint* would be emically described as "opposite-sex sibling" and "younger same-sex sibling", compared to the English *brother* and *sister* which would emically be described as male or female siblings, respectively (Evans, 2010). But, as is seen from the example, emic categorisation does not neatly line-up across languages. In order to do comparative research, we need a language-independent yardstick, which is why the etic approach is a vital tool.

The goal of this database is to contribute to high-level cross-cultural comparison, therefore Kinbank assumes an etic, and genealogical approach. An etic approaches divides relatives into a grid of genealogically defined categories, additionally creating categories based on gender and relative age (e.g. father's elder brother, or sister's daughter). The logically derived grid provides a prototypical referent from which to draw macro- and cross-cultural comparison, and has previously been used to good effect by Nerlove and Romney (Nerlove & Romney, 1967). After first developing an etic grid for sibling terminologies using the three dimensions of sex of referent, sex of speaker, and relative age, they identified a logically possible set of 4,140 terminologies, which gives all possible partitionings of this set. Sampling 240 languages, they found that most of the design space was in fact unpopulated, with just 12 types of sibling systems accounting for 98% of observed cases. Kinbank uses an etic approach to terminology, and therefore a database designed to explore the cross-cultural diversity of kinship terminology.

3.3.0.2 Language sampling

At time of publication, Kinbank holds 183,282 different data points across 1,151 languages. The collaborative approach to this project has built a database with both a broad global sample coupled with focused sampling from specific language families. See figure 3.1 for a map of the distribution of languages.

Parabank is a global project collecting language data on paradigmatic systems: pronoun, verbs, and kinship systems. Kinship terminologies were collected as they became available, including the digitisation of the terminologies within the original kinship survey, *Systems of Consanguinity and Affinity* (Morgan, 1871). The global nature of the Parabank sample means the database holds terminologies from societies experiencing a range of ecological pressures and kinship structures, allowing us to explore convergent patterns of terminology (e.g. Passmore et al., In preparation) and patterns of borrowing between linguistic groups (e.g. Honkola & Jordan, In preparation).

Varikin focused on sampling languages that are paired both with a dated language phylogeny (e.g. Gray et al., 2009) and with existing anthropological databases (e.g. D-PLACE; K. R. Kirby et al., 2016). This sampling of languages is especially amenable to phylogenetic analysis that controls for patterns of autocorrelation that might occur through descent (Jordan & Dunn, 2010). The most sampled language families in Kinbank are Austronesian (n = 375), Atlantic-Congo (117), Indo-European (105), and Pama-Nyungan (104).

All terminology entries are identified by their source publication (book, journal, article, etc.). Some data was primary (i.e. elicited from native speakers), but much came from ethnography, wordlists, and grammars. Each entry is linked to a stable and unique linguistic identifier - "glottocodes" - that are used to link language and cultural data to other databases (e.g. Hammarström, Forkel, & Haspelmath, 2019; K. R. Kirby et al., 2016). By indexing on source, we can also separate terminologies within a language across sources, which allows analyses to measure concordance across sources, track change over time, or identify within-language variation.

3.3.0.3 Concepts / Parameters

The primary search criteria is a core set of 100 kin types (88 consanguinal and 27 affinal). The sampling grid is available in Appendix B, table S3.2. As discussed in chapter 1, kin types (a genealogical position in the prototypical grid) are distinguished from kin terms (the word used to describe one or more genealogical positions). For example: kin types such as *father's brother* and *mother's brother*, are covered by a single kin term *uncle* in English, but by two terms *ah-ta'* and *lake'-she*, in Uncpapa Dakota (USA). The core set encompasses nuclear family, up to grandparents (G^{+2}) and down to grandchildren (G^{-2}), and from parents to their siblings and parent's siblings' children. Affinal terms are collected for spouses, spouses of siblings, and terms for spouse's nuclear family. Within ego's generation and ego's parent's generation, kin types are also included for sex of speaker, relative age, and age of linking relative. This set is

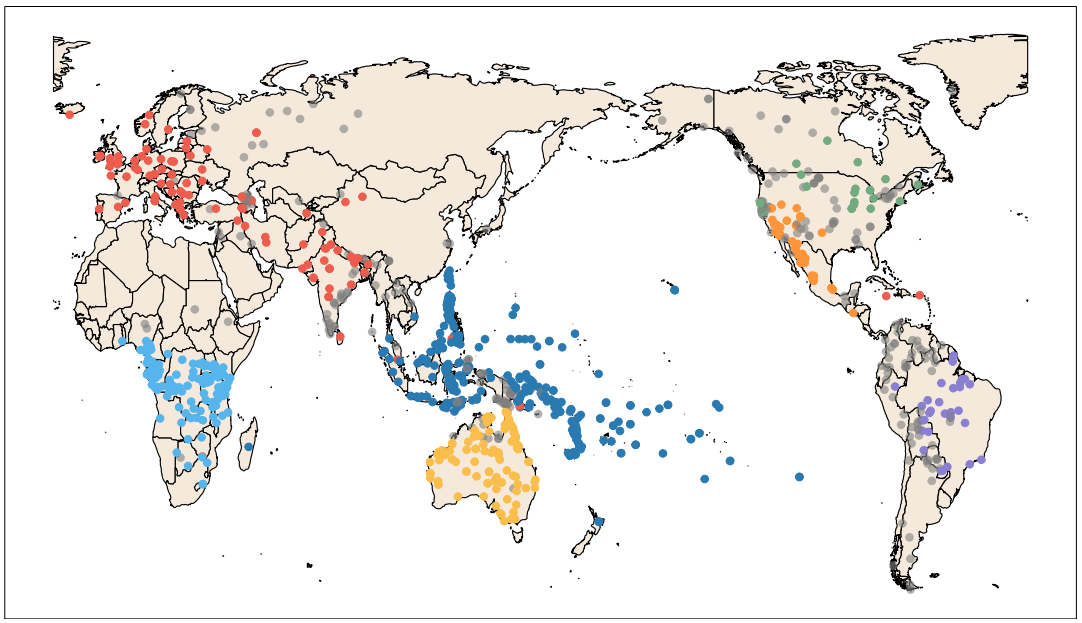


Figure 3.1: Locations of languages in Kinbank. Each point indicates a unique language variety. Coloured points indicate languages from the most populated language families: (from left to right) Bantu (light blue), Indo-European (red), Austronesian (dark blue), Pama-Nyungan (yellow), Uto-Aztecan (orange), Algic (green), Tupian (purple), and other languages (grey).

derived from a genealogical grid of relatives and aims to capture a globally recurrent set of cross-culturally valid kin-members.

The dataset contains terms of reference (the answer to: "who is this person to you"), as opposed to terms of address ("what do you call this person") (Parkin, 1997). Reference terms have more commonly been the focus of anthropological analysis, since these designate formal categories of relationship (e.g. "father" vs "dad"). Terms of address were recorded in adjacent columns when they were easily available but are not the focus of this collection.

Which individuals in our set are designated by kin terms is culturally variable (Barnard, 1978). Some communities have a restricted set of kin terms, and others an expanded set extending beyond the established genealogical grid (Parkin, 1997); however, data collection within Kinbank is emic, inasmuch as I focused on the terms themselves rather than their use for any particular individual relation. In the case of a restricted set, cells that are not required are left empty. This presents the difficult challenge of knowing whether a term is absent because this relative is not consider a kin member, or because it was not recorded. Ultimately this judgement is left to the user. In the case where a language uses kin terms for genealogical relatives outside that of our core set of kin types, new concepts are created as and when they are needed. For example: Hindi uses the term *bābā* for father's father, but the term also incorporates father's father's brother and father's mother's brother (an emic gloss might refer to this category as male elders in a paternal lineage). In this case, the concepts father's

father's brother and father's mother's brother are added to the concept list.

3.3.0.4 Format

Data is stored and distributed in the Cross-Linguistics Data Format (CLDF; Forkel et al., 2018), which is a flat structured database stored in CSV files. This format is easily importable into common analysis tools like Microsoft Excel and data analysis languages like R or python. The key tables in this data model are:

- **Languages:** metadata on each language (longitude, latitude, preferred name, etc.).
- **Parameters:** all the kin types with a written and coded description.
- **Forms:** kin terms and kin types, as well as the identification of the language, parameter and source they are linked to. Within forms, each row is a unique combination of kin term and kin type.
- **Source:** where data was collected from existing sources, the citation is collected, or anonymised native speaker details.

It is common for languages to have multiple terms recorded for particular categories of kin. Due to the combination of form and kin type, the database is flexible to this problem, but it is important to keep this in mind during any analysis. Multiple terms for single kin type may occur for a number of reasons: doculect variation, borrowed and source terms coexisting, unrecorded dialectal differences, confusion of address and reference terms, different registers, or simply language flexibility (Haspelmath & Tadmor, 2009). The database offers no judgement to the specific case, but links to original sources make further investigation accessible for the user.

Kin terms are transcribed as closely as possible to their source form. Since kinship terminologies are predominantly collected by anthropologists and not linguists, sources are primarily in Roman script and are likely to contain coding inconsistencies across languages. Erring on the side of caution, there are no judgements on which transcriptions are correct or incorrect. The database accommodates IPA transcriptions should they be or become available. When a source records the terminology using an alternate script (e.g. Cyrillic), an exception is made and kin terms are transcribed into Roman characters, with the original form held in an adjacent column. This approach means that transcription is consistent within source and within language but may not be consistent across sources or languages.

3.4 Inter-rater reliability

Forty-four languages were collected in both projects, and these are used to determine the level of intercoder reliability. A major avenue for error is when kinship terms are collected

Table 3.1: Structural similarity scores between Parabank and VariKin collections in a set of 44 overlapping languages. The average similarity of the total structure of languages is 0.80, and with a random sample 0.74.

Relationship subset	**Structural similarity**
Complete system	*0.80*
Random sample	*0.74*
Parents	0.89
Children	0.83
Parent's parents	0.79
Parent's sibling's children	0.74
Affines	0.69
Parent's siblings	0.68
Children's children	0.64
Parents Parent's siblings	0.62
Siblings	0.59
Sibling's children	0.42

for one language but two different sources across the projects which disagree on kin terms. Of most interest is ensuring the structural paradigm of a particular kinship terminology is consistent (i.e. that all *parent's female siblings* are syncretised to "aunt" in English). This is what is used to determine inter-coder reliability. To test for structural similarity, all pairs of syncretised kin types within each language are identified within in each collection. This process creates a binarised vector for each language in each database, representing the structure of each language. This vector is used to compare whether the presence or absence of syncretisms are the same across collections in the 44 languages. The sum of matches divided by the total number of pairs gives a measure of structural similarity, where a score of 1 will indicate an exact structural match. Across all compared relationships, this gives us a structural similarity value of 0.80. Taking a random sample of compared relationships gives us a mean value of 0.74 (table 3.1). This score is calculated for various subsets of kin types to check for any focused areas of differences. Amongst the subsets there are high levels of agreement amongst parents, children, parent's parents, parent's sibling's children, but lower levels of agreement between G^{+1} (parents and parents' siblings), siblings, and sibling's children.

In table 3.1, the "complete system" structural similarity score is higher than any subset of kinship terminology: this is because the number of comparisons in the complete system is exponentially higher than any subset. Within this larger number of comparisons, many of are unlikely syncretisms (e.g. between *male speaking father's younger brother* and *female speaking son's wife*), that are not included in any subset. The increase in these types of features results in proportionally more matches, and therefore higher similarity. These results give confidence that Kinbank shows reliable structural similarity. Other proposed errors of kinship terminology transcription include orthographic errors, transcription errors, misinformation,

within-language variability, and linguistic change not accounted for here. It will be difficult to determine the origin of these types of differences across sources, so it is preferable to use within-source comparisons when determining cross-linguistic patterns in kinship structure.

3.5 Are you my *mama*? Nursery words and sound meaning

To demonstrate the usefulness of open source databases to informing linguistic theory, and to highlight the global breadth of the Kinbank sample, I present an analysis testing the relationship between sounds and word meanings in parental kin terms, using a sample of 1,022 languages and across 3,068 kin terms. Previous research on this topic has used samples of 565 (Murdock, 1949) and 1,000 languages (Bancel et al., 2015), and neither case controls for the relatedness between languages. I expand the sample further, and use Kinbank's link to Glottolog by also controlling for ancestral relationships between languages.

The global recurrence of certain sounds in parental terms (mama, papa, tata) amongst geographically distant and historically unrelated languages is widely assumed to stem from early baby babbling, commonly named "nursery words" (Jakobson, 1960). This relationship was first statistically identified by Murdock and subsequently reasoned by Jakobson to recur because of the maximal contrasts the sounds make. The combination of a stop or nasal, followed by a low vowel creates the largest contrast in sound within early babbling and creates recognisable, distinguishable, and identifiable noises, which are good signals for early communication (Jakobson, 1960; Murdock, 1959).

The conservative maximal contrast theory suggests that the limited set of phonetic sounds babies have at an early age, and the maximal contrast of this particular combination of sounds explains the recurrence of babbling parental terms globally (Hendery & McConvell, 2013; Jakobson, 1960). However, in Murdock's tabulations, the [ma] showed a remarkable preponderance with mother, and [pa] or [ta] with father (Murdock, 1959). This led Jakobson to make a further prediction: that mother terms tend to start with [ma] because of the sounds relationship to breastfeeding (Jakobson, 1960). The bilabial nasal sound [m], with an anticipatory murmur, followed by the baby's mouth opening preparing to breastfeed, creates the "ma" sound.

Recent research on Australian languages shows that of the nursery-words commonly used for parental terms; [ma] terms are more frequently used to refer to father rather than mother, and proposes that [ma] is likely to be the ancestral proto-form for father in Pama-Nyungan (Hendery & McConvell, 2013). Hendery and McConvell also show alternative consonants such as [ŋa] (velar nasal) are commonly used for mother, which is still compatible with the breastfeeding hypothesis.

While the effects presented in Murdock's tabulation create a convincing argument for the relationship between [ma] and mother, the evidence from Australia highlights the importance of linguistic history when testing comparative hypothesis. Phylogenetic approaches allow us

to control for these relationships more explicitly when modelling the relationship. Taking the result from Hendery and McConvell (2013) alongside the existing evidence I ask whether there is a statistical link between sounds and kin types in our global sample. Specifically asking whether mother terms more likely to have [ma] or [ŋa] sounds than father terms.

3.5.1 Methods

All words are reduced to the first syllable of their root, following Murdock (1959). This is typically the first syllable of the word, with exceptions being the presence of a prefix, or some other feature of the language which might indicate a different syllable was indicative of the root word. For example the Serbian word for mother is majka: here the first and root syllable is [ma]. Each syllable is then coded for as one of 34 consonant types and one of seven vowel types (following Blasi, Wichmann, Hammarström, Stadler, and Christiansen (2016)). While Kinbank contains similar typographical restrictions to Murdock, due to the fact that most data were not collected by linguists, using a more extensive coding system will capture more linguistic variation.

To control for the relatedness between languages, we coarsely approximate global relationships using the Glottolog taxonomy (Hammarström et al., 2019). We use the approach described in (Roberts, Winters, & Chen, 2015), making the same assumptions of language family depths of 6,000 years and an ultimate depth of 60,000 years. These are not perfect measures of relatedness between languages; however, they are a vast improvement on previously employed methods assuming language independence (see Roberts et al. (2015) for a more detailed discussion on the statistical importance of controlling for linguistic history). All tree manipulation was performed in R using the packages ape v5.3 (Paradis, Claude, & Strimmer, 2004), phangorn v2.5.5 (Schliep, 2011) and phytools v0.7 (Revell, 2012).

3.5.2 Model

I build a phylogenetically-controlled repeated measures multi-level Bayesian logistic regression using brms v2.13 (Bürkner, 2018). By using a repeated measures approach, multiple terms can be modelled per language (e.g. mother and father), while controlling for the phylogenetic relationships between languages. The response is a binary variable indicated whether a term is mother (1) or father (0) and is independently predicted by the consonant and vowel sound codes. I include an inverse variance-covariance matrix built from the tree of relatedness, as well as a random effect for language. This controls for both historical relatedness, and other factors that may be explained at the language level (Bürkner, 2018). Models were run for 4 chains, with 5,000 iterations, and 2,000 burn-in iterations. All fixed effects have normal priors with a mean of zero and standard deviation of ten.

3.5.3 Results

I calculate the probability of vowel-consonant combinations referring to mother from the posterior. Since the model only analyses mother or father words, probabilities close to zero indicate the likelihood a sound refers to father; however, it is also possible that these sounds are used for other close relatives, which are not analysed here (de l'Etang, Bancel, & Ruhlen, 2015). Interestingly, vowel sounds show little preference for mother or father terms, and most variation is explained by the use of consonant. For ease of interpretation, I predict the probability of vowel-consonant combinations which are of theoretical interest: [ma], [na], [ŋa], [pa], and [ta], which are displayed in figure 3.2. A summary of the model and all effects are available in Appendix B, table S3.3. All intervals are 89% high probability density intervals, and intervals that do not contain 0.5 are considered observable effects. There is positive evidence for [ŋa] and [na] referring to mother, and that [pa] and [ta] refer to father. Notably, there is no evidence that [ma] sounds refer preferentially to mother or to father.

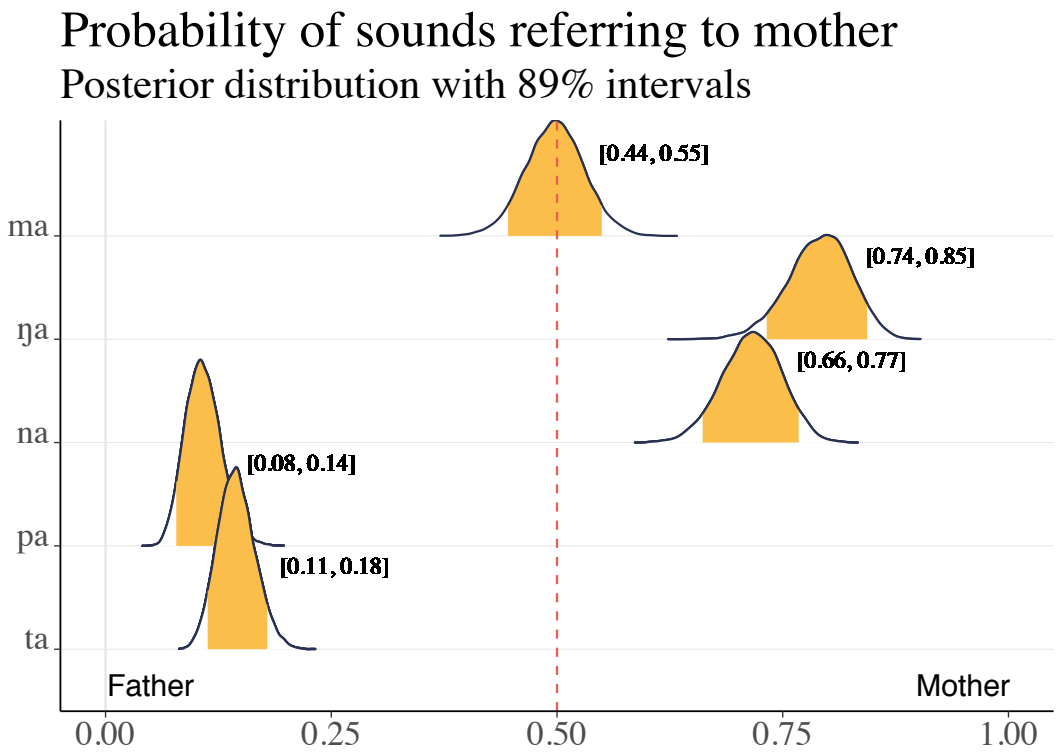


Figure 3.2: Probability of consonant and vowel combinations referring to mother. Each row shows the probability density estimate from the model posterior. Coloured sections and annotated number show 89% high probability density intervals. Intervals that contain 0.5 have no real effect - since there is a 50:50 chance the sound refers to mother or father. Results show words with a root syllable of [ŋa] and [na] are likely to refer to mother and [pa] and [ta] to refer to father. [ma] words are predicted to be used equally between mother and father words.

3.5.4 Discussion

There is strong evidence in a global sample for [ŋa] and [na] sounds aligning with mother terms, as reported by Hendery and McConvell (2013) for Australian languages. Despite the longstanding and widely accepted theories presented by Murdock (1959) and Jakobson (1960), we find no evidence to support the earlier finding, which linked [ma] and mother (Murdock, 1959). Closer inspection of Murdock's tabulations shows very few languages using velar nasal sounds in parental terms, in stark contrast to their relatively high frequency in our broader sample. This suggests that sample used by Murdock was either not globally representative or was coded too coarsely. Equally likely is that the [ma]-mother effect may reflect over-representation of sounds due to closely related languages.

The puzzle yet to be solved is the relationship between [pa], [ta] with father. The mouth movements that babies make before breastfeeding offer a putative mechanism linking mother terms and bilabials; however, there is little understanding for why there might be a pattern for father terms. This is a potential avenue of future research for users of Kinbank.

3.6 Does crossness indicate marriage preferences?

Within anthropology, kinship terms have been said to reflect patterns of social structure, with marriage discussed as the strongest force on linguistic change (Godelier et al., 1998). Here I show how data from Kinbank can be integrated with other databases to test hypotheses about the relationship between language, culture, and behaviour. This example tests for correlated cultural evolution between patterns of crossness in the parental generation and cross-cousin marriage. I use terminological data from Kinbank, cousin-marriage preference data from D-PLACE (K. R. Kirby et al., 2016; Murdock, 1967), and link these data to languages on the Bantu phylogeny (Grollemund et al., 2015) in order to test if these two traits co-evolve together (Pagel & Meade, 2017).

Crossness is when kin relationships are traced through opposite-gender siblings (Parkin, 1997). For example, a cousin who is the child of a father's sister is a cross-cousin because a father's sister is your father's opposite-gender (or crossed-gender) sibling. Anthropological theory identifies two primary types of crossness, Dravidian-type and Iroquois-type (Trautmann & Barnes, 1998). Dravidian-types are explicitly aligned with cross-cousin marriage because crossed relatives are co-lexified with affinal kin (e.g. the same word is used for a mother's brother and spouse's father; Hage (2006)). Iroquois-types also distinguish crossness in parent's siblings and cousins, but consanguineal and affinal relatives are, by definition, linguistically distinct (i.e. there are different terms for a mother's brother and spouse's father). Because of this linguistic separation in *Iroquois-type* we cannot infer a prescription of marriage.

Much has been written about the purpose of crossness in Iroquois-type systems, the most logical conclusion being that a presence of crossness is always linked to the presence of cross-

cousin marriage, but in the case of Iroquois-types, cross-cousin marriage is not prescribed as it is in Dravidian-type (Viveiros de Castro, 1998). If this is the case, then there should be a co-evolutionary relationship between the presence of crossness and allowable cross-cousin marriage (where allowable indicates cross-cousin marriage is allowed, but not prescribed). For a language to be "crossed" it must distinguish the links between same and opposite gender siblings (e.g. between a father's sister and father's brother). A subset of kinship terminology where this terminological marking is revealed is in the parental generation, specifically within a bifurcate merging organisation, where same-sex siblings are merged, and crossed relatives are distinct ($F = FB \neq MB$ and $M = MZ \neq FZ$). I then hypothesis that allowable cross-cousin marriage should co-evolve with a bifurcate merging pattern.

Within the Bantu language family, cross-cousin marriage occurs in 38% of societies, but Dravidian-style terminology in contemporary languages are rare (Hage, 2006; K. R. Kirby et al., 2016). Historical linguists have previously reasoned the likely Proto-East-Bantu parental kinship terminology contained a Dravidian pattern, which may explain the persistence of cross-cousin marriage in this sub-group, but does not offer help explain the presence of cross-cousin marriage in the broader Bantu family (Godelier, 2012; Marck, Hage, Bostoen, & Muzenga, 2010). The link between bifurcate merging terminology and matrimonial exchange then, offers an explanation for this discrepancy.

3.6.1 Methods

I use a Bayesian correlated evolution phylogenetic approach, implemented in BayesTraits v3.0.1 (Pagel & Meade, 2017) to test the relationship between the presence of cross-cousin marriage and the presence of bifurcate merging terminology. By using a Bayesian approach with a sample of phylogenetic trees, the model does not only control for shared ancestry between societies but for the uncertainty in the phylogenetic relationship.

The cross-section of Kinbank and D-PLACE results in a set of 56 societies for which Kinbank contains kin terms for all parents and parents siblings, information on the practice of cousin marriage in that society and can be linked to taxa on a dated Bantu phylogeny.

Kin term data is coded for the presence or absence of a bifurcate-merging pattern in each of the male and female relatives in the parental generation, exemplified by the following rules:

$$F = FB \neq MB$$

$$M = MZ \neq FZ$$

This pattern is often strictly followed; however, it is common in sub-Saharan Africa for parent's same-sex siblings to be terminologically equivalent but distinguished by age through terms such as "big" and "little" parent. For example, in Swahili, father is *baba* and father's elder brother is *baba mkubwa* (McGrath & Marten, 2015). Languages making these terminological

distinctions are also coded as instances of bifurcate merging, provided there is a distinct MB term. Coding for these patterns by gender created three binary variables: presence of bifurcate merging in men, in women, and complete bifurcate merging. Although there was no pre-existing theoretical reason for making the male / female distinction it became clear while coding that merging patterns are not always symmetrical across sexes, so they are conservatively analysed separately and together.

Data on allowable cross-cousin marriage is taken from the Ethnographic atlas question *EA023: Cousin marriage permitted*. This variable contains thirteen categories of allowable cousin-marriage (including no cousin marriage), seven of which relate to various forms of cross-cousin marriage which I derive an allowable cross-cousin marriage binary variable (EA023 codes: 1-6 and 9; see Appendix B table S3.4 for a coding table). In summary, I perform three statistical tests between a single cross-cousin marriage variable and three merging variables.

For each statistical test there are two models: one model where correlated evolution is assumed, and one where traits evolve independently. These models are compared to calculate a log Bayes Factor (BF) to determine which model best fits the data. BF < 2 indicates weak evidence, > 2 positive evidence, 5-10 strong evidence, and >10 very strong evidence (Kass & Raftery, 1995). All models are run for 10,010,000 iterations, sampling every 1,000 iterations, with a burn-in of 10,000 iterations, on a posterior sample of 100 trees (approximately 200 samples per tree). Each model was run twice to assess convergence, all parameters have an exponential prior with a mean of 10.

3.6.2 Results

There is no evidence for the co-evolution of cross-cousin marriage and bifurcate merging terminology in any of the three variables. In the *complete bifurcate merging*, and *bifurcate merging in women* tests there is no evidence for or against the co-evolution of cross-cousin marriage and bifurcate merging organisations (Complete log Bayes Factor = -0.83; Women: -0.18). Whereas in the *bifurcate merging in men* variable there is positive evidence of independent evolution (log Bayes Factor = -2.28), suggesting in this set of data bifurcate merging terminology have no general relationship to cross-cousin marriage. Figure 3.3 displays the data for the complete bifurcate merging variable on the Bantu phylogeny. The internal nodes, which are probabilistic pie-charts for each state, show confidence in relatively recent changes, but is very uncertain about change in the deeper nodes. The confidence in recent changes highlight the frequent gain and loss of cross-cousin marriage, but without the change of kinship terminology. Why the model expects such frequent change in cousin marriage, but not in terminology is an avenue for future exploration. Since the model was inconclusive in two variables, an increased data set may also improve our understanding of this relationship.

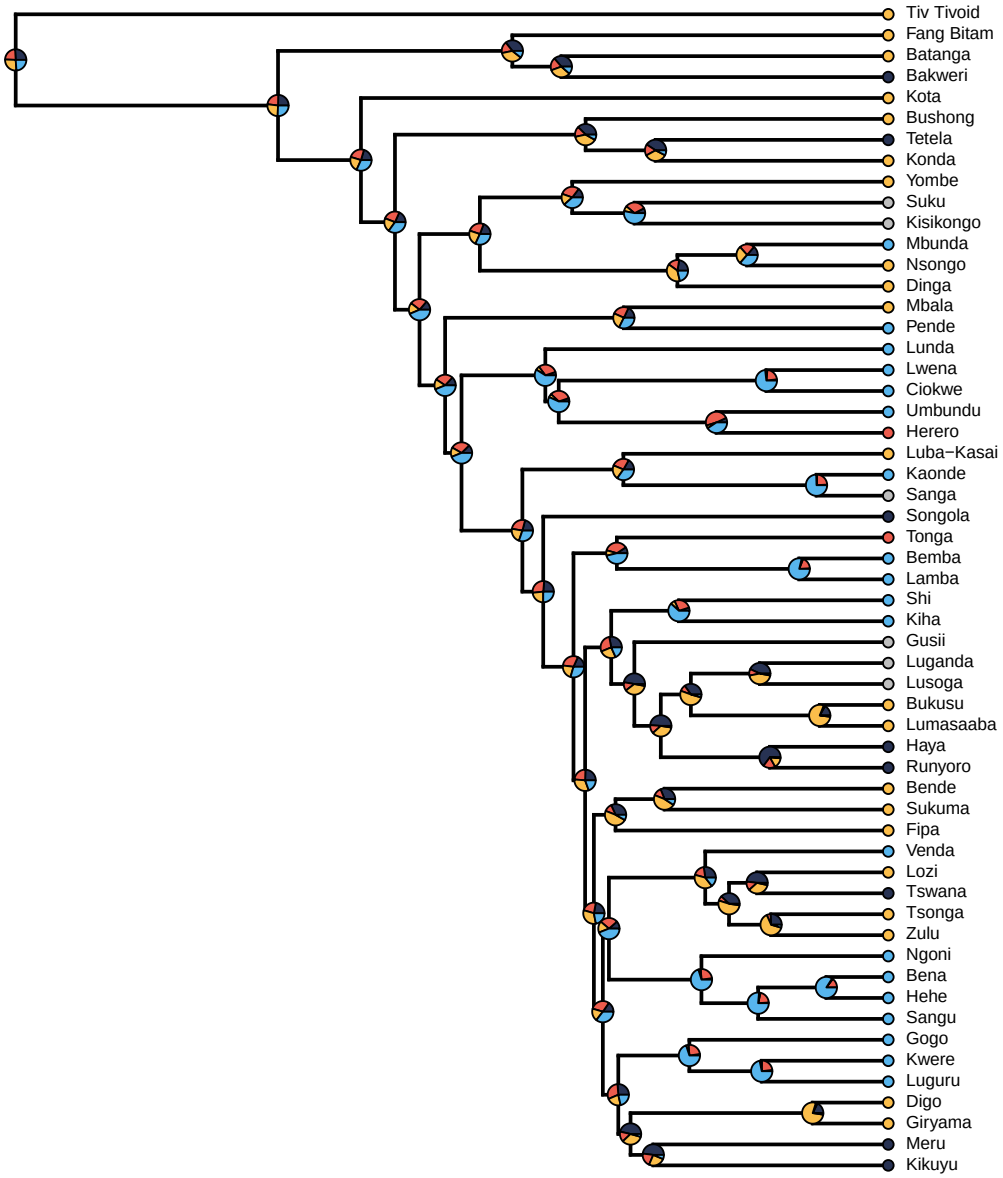


Figure 3.3: Maximum clade credibility Bantu tree displaying four possible states: No cross-cousin marriage and no crossness of kin terms (dark blue), no cross-cousin marriage with crossness (yellow), cross-cousin marriage and no crossness (red), both cross-cousin marriage and crossness are present (light blue), and their likely probabilities from a dependent model of evolution. Grey indicates missing kin term data. Pie-graphs indicate the probability of states at each node, and are recreated through BayesTraits RecNode functionality. Evidence of the independent evolution can be seen through the frequent pairing of red and light blue, and yellow and dark blue - representing the gain and loss of cross-cousin marriage, without any linguistic change. Deeper into the phylogeny there is much uncertainty as to the relationship between these two traits, indicated by the equal probability of all four states.

3.6.3 Discussion

The relationship between crossness in G^{+1} and cross-cousin marriage is inconclusive from this analysis, placing a question mark over a fundamental relationship between kinship terminology and social behaviours. Marriage practices are widely considered a primary structural driver of kinship terminology, so finding no evidence of cross-cousin marriage influencing G^{+1} terminology presents a considerable dent in the theoretical foundations of this theory (Parkin, 2012).

Kinship theory has explored many possibilities in the link between language and behaviour, but the mounting exceptions to the "rules" (e.g. Guillon & Mace, 2016, See chapter 2), suggests that any particular kinship terminological organisation might reflect the solution to more than one social problem. If kin terms are considered cultural categories, with accompanying behavioural expectations, it may be the case that societies can arrive at the same structural organisation but with each category conveying culturally specific meaning. Two ethnographic examples from our dataset help illustrate this. The Bena people (Tanzania) who used linguistic crossness, allow, but do not prescribe, cross-cousin marriage, and practice polygyny (Culwick, Culwick, & Kiwanga, 1935). Amongst the Bena, the distinction of cross-cousins reflects the predicted relationships between marriageable and non-marriageable cousins. Cross-cousin marriage is considered a high-status marriage, although other marriages frequently occur. The category of cross-cousin in the Bena is large, and could stem from a cross-cousin relationship from many generations before (e.g. FFFZ offspring), and the closer the relationship, or if the relationship is traced through a person of high status, the more status the children of that marriage begin with.

In contrast, the Lumasaaba (Western Kenya), used linguistic crossness, but have no cross-cousin marriage preference. Amongst the Lumasaaba, parent's opposite sex siblings play important roles in a child's life (Heald, 1989). The importance of these relatives in rites of passage ceremonies, and being primary route of inheritance norms (until recently) highlights a special relationship between children and their mother's brother or father's sister, which could be the cause of the linguistic distinction. These are speculative examples taken from our sample, but the relationship of kinship terminology structure to various semantic meanings is an avenue for future research.

3.7 Conclusion

Kinbank offers an open and transparent database of kinship terminologies from a global sample of 1,151 languages. The digitisation and centralisation of kinship terminology opens the door for large scale comparative work on kinship terminology, across a number of fields such as linguistics, anthropology, and cognitive sciences (Evans, 2010; Jordan, 2011; Kemp & Regier, 2012). This database already contains a large number of languages and sources, and the open format allows the database to improve and grow over time.

The examples have shown the benefit of open-source databases to answer questions in linguistic and anthropological theory, and how the phylogenetic sampling allows for the application of new methodological approaches. The study of kinship and kinship terminology has long been a topic of interest, and establishing this database can encourage important and interesting work on kinship and its role in cultural diversity to continue.

Chapter 4

Kinspace: Re-conceptualising kinship terminology diversity

4.1 Kinship terminology and diversity

In the previous chapters I have established that kinship terminology is a complex and diverse domain, and highlighted the biological, social, and cognitive constraints to its diversity found in existing literature (Jones, 2010; Kemp & Regier, 2012). While some anthropologists reason that kinship terminology diversity is likely to be low, centring around a few key types (Godelier, 2012), I showed in chapter 2 that the existing six-piece typology has little analytical value. The six-piece typology is developed from the top-down, by combining rules of collaterality, bifurcation, and generational skewing (see section 1.2). The top-down approach to typology offers a broad-brush interpretation of diversity, but ignores swathes of information by focusing on particular traits to represent the entirety of a terminology. In chapter 3, I use two alternative approaches, by analysing kin terms individually (section 3.5), or by categorising kinship terminology into the presence or absence of a particular feature (section 3.6). These approaches are more granular than a typological approach, but inherently restrict diversity to a domain of interest. This chapter aims to explore the totality of kinship diversity from the bottom, up, by conceptualising terminology similarity within a metaphorical morphospatial approach.

Previous bottom-up research has derived the combinatorial possibilities of a set of theoretically possible kin types to determine the totality of diversity, and then reduces this set using logical and theoretical reasoning to a typology (e.g. Lowie, 1928; Nerlove & Romney, 1967). Both Nerlove and Romney (1967) and Lowie (1928) identify the number of logically possible combinations for siblings and G^{+1} respectively, and from this set of possibilities use layers of rules such as the preferences for conjunctive categories (Nerlove & Romney, 1967) or the rule of collaterality (maternal relatives can only be merged with lineal relative if paternal relatives are as well; identified by Héritier, 1981) to determine a set of tractable possibilities.

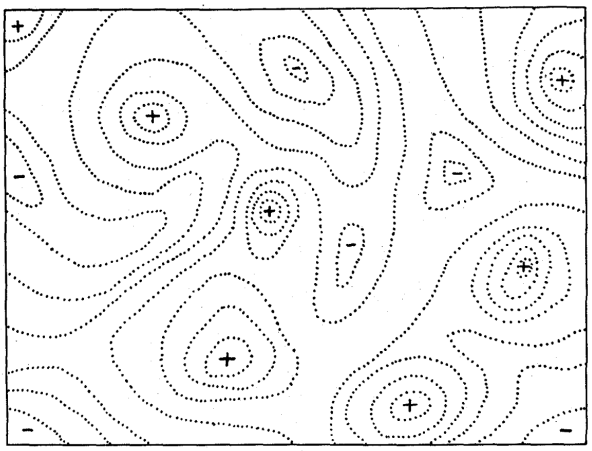


Figure 4.1: The original caption reads: "Diagrammatic representations of the field of gene combinations in two dimensions instead of many thousands. Dotted lines represent contours with respect to adaptiveness" (Wright, 1932, p. 358). Additionally, a "+" indicates a fitness peak, and therefore a desirable gene combination, and "-" indicates a trough. This conceptual approach to gene and species fitness, helps conceptualise why certain gene combinations outperform others, resulting in the differential survival of genes and species.

The success of these approaches is in their reproducibility, and shows that in developing a typological framework for kinship terminology it is important to first establish the largest possible frame of diversity. Here, I used the idea of maximal diversity to develop a conceptual kinship morphospace, or *kinspace*.

In contemporary literature, morphospace is more commonly used as an analytical tool, but has also historically been used in a metaphorical sense (Mitteroecker & Huttegger, 2009). In biology, morphospace has been used to identify clusters of phenotypic similarity between, or within, species. For example: the position of bird species within a phenotypic morphospace derived from their physical features was predictive of major niche conditions, such as its position in the food chain, dietary resource type (e.g. herbivores, pollinators or predators) and fine-scale variation in foraging behaviour (e.g. catching insects in flight, from vegetation, or the ground) (Pigot et al., 2020). As a metaphor, when geneticists began to realise the enormous combinatorial possibilities of genetic variation for even a small set of alleles, Wright (1932) introduced the idea of a *fitness landscape* as a way to understand the differential survival of genes and species, and how mutations change this landscape and therefore survival (see figure 4.1). In this two dimensional space, each axis represents the combination of two alleles, and contour lines highlight the adaptiveness of that combination (figure 4.1). Using a morphospatial approach reduces the complexity of multiple comparison into a single conceptual framework in which to understand the problem.

Within cultural (Burton et al., 1996; Kapitány, Kavanagh, & Whitehouse, 2020), and cognitive (Majid, Boster, & Bowerman, 2008) contexts, morphospatial approaches have been used to

determine patterns of cross-cultural similarity. In the cultural context, morphospaces have revealed the seven key dimensions of human ritual, ranging from dysphoric and euphoric elements of ritual, to physical and psychological pageantry (Kapitány et al., 2020). A morphospatial approach to societal construction revealed that descent practices, and matri- or patricentricity are key components of cross-cultural differences in human society (Burton et al., 1996). In cognitive research, morphospace helped estimates the cognitive and linguistic space of cutting and breaking events, finding considerable cross-cultural similarity within this semantic domain (Majid et al., 2008).

In this chapter, I utilise morphospace in the metaphorical sense, and in the next chapter I will approximate the ideas discussed in this chapter with quantitative methods. By using a morphospatial approach, high levels of diversity can be understood in a manageable framework, using existing theoretical reasoning to shape the structure of the space (Mitteroecker & Huttegger, 2009). Morphospatial approaches also impose interesting questions unanswered by existing theory, such as how distance relates to similarity, and how similarity relates to change (Mitteroecker & Huttegger, 2009). Using the assumptions imposed by a spatial understanding of diversity, when considered in relation to existing literature, will help us understand the current state of kinship diversity literature, but also raise new and interesting theoretical questions.

4.2 A new approach to kinship terminology diversity

To develop a spatial framework of kinship diversity it is necessary to establish the unit of analysis and define the relationship between these points. As with biologically formed morphospaces, each point indicates a particular organism or unit (Mitteroecker & Huttegger, 2009). Here, a unit is a possible organisation of a terminology, which may or may not be attested in the ethnographic record. The space is organised by a similarity distance, where a small distance indicates more similarity. I discuss distance in more detail in section 4.2.5, but as a brief example: within kinspace the cousin terminology used by English and French would be close to each other. Both have gendered terms for siblings, and group all cousins under a single category. French additionally distinguishes cousins by gender. The gender distinction makes the organisations close in the morphospace, but not identical. Māori kinship terminology collapses cousins and siblings terms and in parallel the meaning of these terms (see figure 1.1). Since Māori organisation is quite different to English or French, it would sit further away in the morphospace. The example only compares cousin terms, but conceptually this restriction is unnecessary and a measure of similarity could incorporate all possible similarities and differences across languages (categorical, sound, semantics, syntactic; Hock & Joseph, 2019). Applying a function of similarity to all possible kinship terminology places all organisations at a point relative to each other, and in doing so, creates a morphospace of kinship diversity.

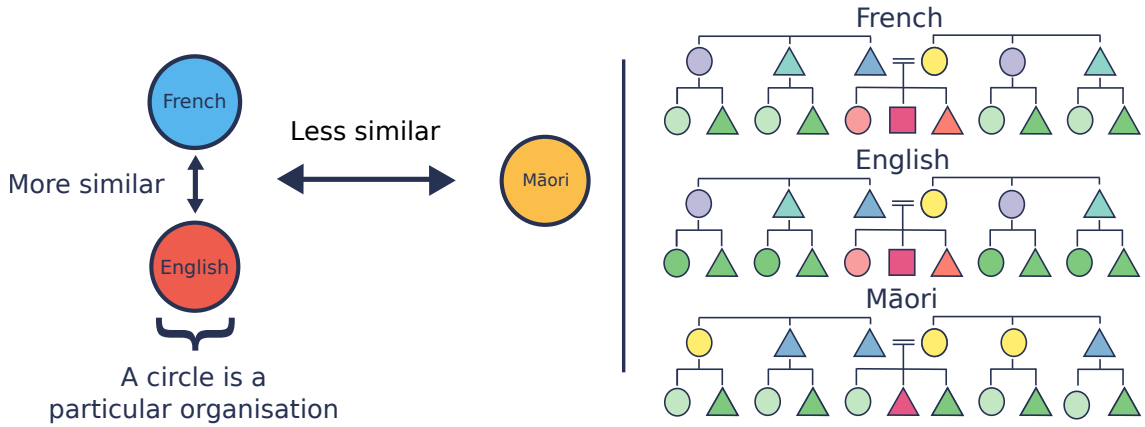


Figure 4.2: *Left:* An example of what kinspace might look like. Each circle is a particular organisation. Distance between circles indicates similarity. English and French are similar, because the difference between them is small (gendered vs un-gendered cousins). Māori is further away since all cousins and siblings are collapsed under a single term. *Right:* The terminology for each language in the example. Colours indicate common terms. For example, all cousins and siblings are green in the Hawaiian system.

The idea of kinspace is conceptually similar to some existing approaches to kinship terminology analysis, such as the kinship hyper-cube used to understand types of crossness (Tjon Sie Fat, 2018) and in the relationship between terminology and social structure (Whiting, Burton, Romney, Moore, & White, 1988). The development of the hyper-cube stems from the same concerns established in this thesis, that the six-piece typology does not sufficiently represent diversity (section 2.4). The hyper-cube is specifically concerned with diversity in types of crossness (that is, terminology akin to Iroquois- and Dravidian-style organisation; see section 1.1.2). The hyper-cube connects sixteen logical possibilities of crossness in a four-dimensional space (see figure 4.3). The connections between the logical possibilities indicate a structural change in terminology, and immediate neighbours are proposed "next-steps" in the evolutionary change. This is similar to the networked model of change I will propose in section 4.2.5.

In an empirical approach to kinship terminology and morphospace, Whiting et al. (1988) coded kinship terminologies across a number of features (e.g. is there one word for grandchildren (1) or are there gendered terms for grandchildren (0)), alongside societal level variables (e.g. does a society practice monogamy, polygyny, or sororal polygyny), and projects each of these datasets into space. The terminology and societal morphospaces were compared to find that particular kinship terminologies often align with particular social structures. For example: Omaha- and Crow-style cousin terms sit close to the patrilineal and matrilineal structures, as existing theory would predict (Goody, 1970). But also that terminology overlapped significantly with multiple societal clusters, such as Iroquois-style cousin terms close to both matrilineal and patrilineal societal clusters. The projection of kinship terminology into a multi-dimensional space is similar to the quantitative approach kinspace in the next chapter.

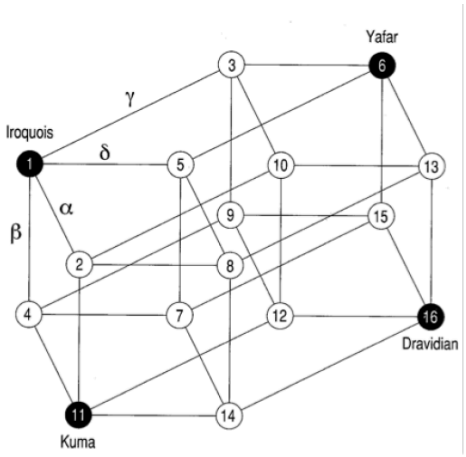


Figure 4.3: Figure taken from Godelier et al. (1998). This shows the hyper-cube used to understand the 16 possible variants of crossness, of which four are linked directly to observed societies (indicate by names in the figure). Each circle indicates a particular organisation, and each vertices indicates a reversal in a feature of crossness (Tjon Sie Fat, 2018). There are 24 different paths of change, and a minimum of four steps between the most commonly observed forms of crossness, *Iroquois-type* and *Dravidian-type*. Greek letters indicate which kin types are crossed: α is same-gender cousins and same-gender child, β is same-gender cousins and opposite gender child, γ is opposite gender cousins and same-gender child, and σ is opposite-gender cousins and opposite-gender child.

Drawing inspiration from Godelier et al. (1998) and Whiting et al. (1988), I extend kinship terminology space to all theoretical diversity in kinship organisation, using generative approaches, such as: Optimality theory (Jones, 2010), and kinship algebra (Read, 2013), to develop their relationship in space (introduced in section 1.2.2). The morphospatial representation of diversity introduces the basic principle of kinspace, and in the following sections I discuss the various implications of considering diversity in this way.

First, I discuss the size of the space. Most combinatorial approaches to kinship terminology begin with a set of kin types, which inherently creates an upper limit on possible diversity but underestimates the true diversity in terminology. Here, using a genealogical and social definition of kinship, I argue that kinship terminology still has a finite set of organisations (although exceedingly large). Genealogical kin refers to the relationships created through reproductive ties, where social kinship indicates kin who are only defined as kin through to cultural norms. Second, I discuss how existing typologies can inform the topography of kinspace and indicate likely clusters of observed terminology, how distance between clusters can inform models of change, and whether clusters are equally variable. Finally, I consider how the space changes over time, and what evolutionary forces might predict that change.

4.2.1 Limits of Kinspace

A theoretically interesting question is whether the number of possible kinship terminology is finite, or whether there are always new possibilities in kinship terminologies? When considering this in terms of kinspace, I am asking whether it is possible to count every point in space, or are there infinite points. Whether kinspace is finite or not is an important constraint to establish, because if there is finite variation, all possibilities are knowable and therefore explainable, whereas if this assumption cannot be made, all theories must be robust to new and unknown variants. Which one of these assertions is correct influences the analytical approach that should be taken when understanding terminology diversity. For kinship terminology organisation to be finite, the definition of who is and who is not kin must be bounded. Intuitively, there must be some upper limit because there a limit to the number of individuals anyone person can know (discussed more below). But this appears to be the exception rather than the rule. If there is a finite set of kin, then the number of possible ways to organise that kin is by definition, also finite.

Kinship terminology is easily defined as finite for any predefined set of kin types. This was famously identified by Nerlove and Romney (1967) who identify 4,140 possible[1] organisations for eight sibling terms, and use theory to develop a 12-piece typology. However, it is slightly more complicated to reason that all kinship terminology variation is ultimately finite, since the complete set of relatives considered kin varies between societies (Parkin, 1997). Previous research has described this as kinship *range* (Barnard, 1978). Range indicates how widely, or how narrowly, kin is defined within a particular society. If all members of a society are considered kin, that society is considered to have maximum, or universal, range. Universal range encompasses both social and genealogically defined kin, whereas other societies have a strictly genealogically definition of kin.

Cross-cultural variance in range means that for any pair of languages, the combinatorial possibilities are not necessarily equivalent when considering the culturally relative set of kin. For example, Altaic speakers in Mongolia have no terms for paternal cross-cousin and these relatives are not considered kin (Krader, 1953). The exclusion of paternal cross-cousin from the kin group is attributed to patterns of patrilineal exogamy and patrilocal residence, which takes fathers sister away from their natal home and raised apart from the rest of the kin group. However, western and industrialised societies often consider fathers sisters children as close kin (e.g. France, U.K.). Including paternal cross-cousins as kin means there are 3,937 more possibilities in cousin organisation in a European language, than within Altaic languages.[2]

The recent application of cultural evolution to kinship and kinship terminology has high-

[1] This is the eighth Bell number. Bell numbers indicate the set of combinatorial possibilities for any number of items.

[2] Since paternal cross-cousins are not considered kin, Altaic groups only have six cousin types (FBC, MZC, MBC), where as English (for example) has eight. The sixth Bell number is 203, and the eighth is 4,140. $4,140 - 203 = 3,937$

lighted the importance of history in the evolution of kinship terminology, suggesting that culture-specific constraints will influence change over time (Jordan & Dunn, 2010). This could encompass change in who is, and who is not kin, suggesting that the theoretical possibilities of kinship terminology is variable over time, within a language. This change is seen between Old English, which does not contain specific first-cousin terms, to Modern English, which does (L. Lancaster, 1958).[3]

To reason that the number of theoretically possible kinship terminology are finite, we must also reason that who is and who is not kin is a bounded set. This set is likely to vary between languages and over time. By establishing who is and who is not kin as finite, then by function of that set, there is a finite number of possible kinship terminology.

4.2.2 Kin as a finite set

Defining who kin are is an ongoing debate between different anthropological traditions (McKinnon & Silverman, 2005; Shapiro, 2008). As set out in the introduction (see section 1.1.1), cross-cultural anthropologists have tended to analyse sets of genealogical kin, since the genealogical grid creates a prototypical platform for comparison across languages and cultures. Social anthropologists have preferred to study the concept of "relatedness" which is more flexible with regards to the cross-cultural variation of social relationships found within any particular group (Carsten, 2004). In an attempt to reconcile these two positions I use a broad definition of kinship which encompasses the combination of genealogical underpinnings, social rank, and group membership (Jones, 2003a). This definition aims to incorporate both the genealogical connections dictated by reproduction, but also the purely social elements of kinship. In the past there have been debates between the importance of either genealogically based kinship or culturally-relative approaches to kinship, modern theories highlight that terminologies are derived from the interaction of these domains and analyse them in parallel - exemplified by kinship algebra (Read, 2013).

To define the number of kinship terminology organisations as finite, it is necessary to reason that both genealogical distance and group membership are restricted to a finite number of people, assuming social rank is constrained to individuals within these groups. The genealogical restrictions on "who are kin" stem from biological theories of kin selection, suggesting that as genealogical distance increases the likelihood that an individual will cooperate with a relative decreases (Hamilton, 1964). Across a variety of domains there is both experimental (Bacha-Trams et al., 2017; DeBruine, Jones, Little, & Perrett, 2008) and observational (Jankowiak & Diderich, 2000; M. S. Smith, Kish, & Crawford, 1987) evidence of kin-selection influencing

[3]While there was no specific kin terms for first-cousin in Old English, there were terms, such as *mægo*, which glossed to kinsman in which they would be incorporated. So, strictly speaking first cousins were considered kin, but were categorised as a general and more distant category of kin that we might attribute them to today (L. Lancaster, 1958). However, this still example still highlights variability in which kin are incorporated in kinship terminology, and which are not.

behaviour in humans. While there is no theoretical limit to how small genealogical distance can become, there becomes a point where theoretical level of genetic overlap between relatives falls below average genetic relatedness within the broader population. The threshold of relatedness between kin and the general population offers a natural upper limit of who kin are from a purely genetic perspective. Within Europe, average genetic relatedness of national populations ranges between 0.4% and 1.8% of shared DNA, which would place this limit between (using English categorisation) fourth cousin and second cousin once removed (Ralph & Coop, 2013). We might observe variation in this genealogical limit in a global sample, but we can establish a theoretical upper limit as when average population relatedness is greater than average shared genes in relatives.[4]

From a social perspective, human groups draw a distinction between in-group and out-group members, and similarly between kin and non-kin (Jones, 2018; McElreath, Boyd, & Richerson, 2003). As human groups vary in how they are organised and marked against each other (Barth, 1998), they also vary in the definition of who is, and who is not kin. While a biological approach to kinship emphasise the genealogical distance between individuals, a long tradition in social anthropology proposes kin relatedness extends beyond this, with particular focus on relatedness and how that is experienced through "the house" (Carsten, 2000). The house, also strongly linked to the hearth, in this context refers to the experiences of family within a home. By focusing on the lived experience of kinship within the home, this culturally relative approach focuses on the creation of kinship ties, and how relationship are created through shared experience, without assuming ties based on underlying biological factors (Carsten, 2004).

Social definitions of kinship, or *social range*, interact with kinship terminology in two ways: first, by defining the breadth of genealogical relatives considered kin, and second by including non-genealogical kin. A theoretical limit on the breadth of cultural kinship in relation to genealogy can be defined in the same way as the genealogical limit defined above: when cultural relatedness is below that of the cultural relatedness to the average population (i.e. where is the line between someone being a friend or a family member). Social range is much more variable than a genealogical definition of kin: it can be narrower than the genealogical definition, as described in Altaic groups above, can encompass much broader relationships, as seen in the universal range in many Australian Pama-Nyungan kinship systems (McConvell, 2018), or genealogy can be the an important force behind the socialisation of kin, as in English society (A. M. Kramer, 2011).

It is also common to see kin terms used to emphasise the extended family. In Tongan, kin terms are merged for same-sex siblings and same-sex cousins, grouping individuals of different genealogical distances, but also kin terms are often extended to any in-group child of ego's

[4]One area of kin construction where genealogical constraints are entirely absent is in the construction of fictive families. This is an important area of research, and one that is not considered enough here or more broadly in the study of kinship terminology. However, this would require a significant detour in this thesis so we have chosen to omit this particular complexity.

generation (Völkel, 2016). Here, kin terms are viewed as social categories, and categories of kin have prescribed patterns of behaviour (see chapter 6 for a discussion of this). Categories of kin which contain relatives of multiple genealogical distances contrasts with how biological traditions define relatedness, alongside predictions of expected behaviour (Hamilton, 1964). The extension of kin terms to more distantly related or unrelated individuals creates a broader genealogical definition of kin than within Altaic and European societies (Shapiro, 2012).

Some groups drop the egocentric genealogical approach to kinship and use "sociocentric" categories of kin (Brison, 2001). Sociocentric kinship categories become properties of the individual and all individuals within a community or clan are placed into a category (Allen, 2014). These categories then have their own structural relationship, dictating cultural norms of behaviour and respect. This is opposed to the egocentric kinship, where each individual has a unique kin network. The sociocentric nature of kinship is exemplified by groups in Aboriginal Australia who define kinship both in terms of kin and "skin", where skin is the sociocentric categories used within a group (McConvell, 2018). The skin category is a property of that person, for example: in Gurindji an individual who is *jampinjina* is classified as brother to other *jampinjina*, and father to the categories of *jangala* and *nangala*. Importantly however, sociocentric categories are only applicable to group members, and not to everyone.

The social construction of kinship is a complicated concept to unpack, and much time has been spent debating the relative importance of social and genealogical approaches, whether they are even arguing the same point (Parkin, 2009), or how they might interact (Jones, 2018). Fortunately for the argument being made here, it is only necessary to understand that there is an ultimate divide between the cultural definition of kin- and non-kin. An individual can be more or less part of a group (e.g. a leader might be more tied to a group than a peripheral member) and, as with genealogical distance, there will be an ultimate limit where an individual is no more a group member than a stranger. Establishing that only group-members can be (but do not have to be) kin establishes a theoretical upper limit to socially defined kin.

This definition of social kinship creates a bounded group, but, unlike genealogical relationships, has no externally enforced constraint to stop the bounded group theoretically encompassing everyone. That is, the limits of genetic relatedness are imposed through external biological constraints. Groups are defined by humans for humans, and therefore have no external constraint to impose an upper bound. Grounding this idea in human behaviour, research suggests that we have always observed some limit to in-group membership. Social networks are thought to range between 120 and 150 individuals, so societies without universal range kinship are likely to define kin within this limit (R. A. Hill & Dunbar, 2003). Societies with universal range could feasibly consider people kin who are beyond direct links in their social network. For example: amongst the Murrinhpatha in Australia, all community members have allocated kin terms, but as the size of the community grew it became necessary to triangulate the use of kin terms via a linking relative when two individuals were unknown to each other (Blythe, Tun-

muck, Mitchell, & Rácz, in press). The maximum group size for humans is currently unknown, but we can safely assume that it does not and has not encompassed everyone.

Unlike the stability of genealogical links, definitions of social kin-group membership are temporally variable, as well as varying in their importance. Amongst the Belau in the Pacific, there is a flexibility between descent group membership based on the availability of land amongst various groups (McCutcheon, 1981). Whereas amongst the Nuer, patrilineal descent patterns strictly define group membership (Evans-Pritchard, 1940). This complicates how we understand changes in kin terminology over time, which is discussed more in section 4.2.5.

As both genealogical and sociological kin can be defined as bounded groups, it reasons that the union of these two limits creates a finite set of who is and who is not kin cross-culturally. Under this definition, individuals who are more related to an ego than the general population can be considered kin, as well as those who fulfil the group membership criteria. This bounded set creates a finite number of possible terminological organisations.

4.2.3 Topography of Kinspace

After establishing a finite space of kinship terminology, I turn to how languages might be distributed throughout it, recalling that points in space represent a unique kinship terminology, and distance between points indicate is representative of similarity. In addition to this, I introduce the idea that positions in space can be filled or empty, indicating whether a particular kinship terminology is observed or not. Cognitive research, as discussed in section 1.2, has already established that kinship terminology trades off between disjunctiveness and simplicity. Since a large proportion of theoretically defined kinship terminology violate this rule, most of the positions within kinspace should be empty, resulting in a sparsely populated space. What the rest of this section is primarily concerned with is how observed diversity is structured.

Godelier famously proposed there were "very few types ... only ten or so" of kinship terminology (Godelier, 2012, p. 180). Taking this quote literally, there should only be ten observed points in kinspace in an otherwise empty universe. This is an unlikely scenario, as if we strictly account for all kinship terminology variation, we observe more than ten types in Europe alone (Parkin, 2015). To illustrate, there are three different organisations between French, English, and Italian. Where French and Italian use gendered cousin terms (French: *cousin*, *cousine*; Italian: *cugina*, *cugino*) and English does not, and Italian uses generational skewing between niblings (children of your siblings) and grandchildren (nephew and grandson = *nipote*), where French and English do not.

A more generous interpretation might conclude that there are only ten primary distinctions, each of which contain some amount of variation. A primary distinction can be defined as a feature that broadly divides kin types into categories; rules that split this set into smaller subsets are dubbed secondary rules, dividing these subset further are tertiary rules, and so on (Nerlove & Romney, 1967). Outside of the commonly used six-piece kinship typology, variation

is often explained in terms of ordered rules - this is exemplified by the recent application of Optimality Theory (OT) to kinship terminology (discussed in section 1.2.2), but also used in other approaches of kinship terminology diversity (Jones, 2010; Kroeber, 1909; Murdock, 1949; Nerlove & Romney, 1967). By incorporating layers of variation into a physical space, we could observe these ten types as graded clouds of similarity, where all organisations within a cloud follow a primary rule but their placement within a cloud shows localised variation. The extensive ethnographic literature surrounding kinship suggests this is a more likely scenario, and is a common admission of typologists (Lowie, 1928; R. J. Smith, 1962). If these graded clouds of similarity can be observed, they would represent the "cultural elbows" that should be used to develop a typology of kinship organisation (Kronenfeld, 2006). What needs to be established, is whether these clouds align with existing typologies, or divide the space in different ways.

Historically, small differences in kinship terminology have caused much confusion, but are now seen as critical in understanding the relationship between language and behaviour (Lounsbury, 1964; Trautmann & Whitely, 2012). For example, Dravidian-types and Iroquois-types were mistaken for each other, due to identical organisation within G^0 and G^{+1}, but outside of these relatives, there are important distinctions that make Dravidian-types inherently linked with cross-cousin marriage, and not directly linked with Iroquois-types (Godelier et al., 1998). A specific example is the co-lexification between ego's cross-cousins and ego's spouse in Dravidian-type, which highlights the structural relationship between Dravidian kinship terminology and cross-cousin marriage. Similarly parent's opposite-gendered sibling is co-lexified with parent-in-law, cross-cousin's children with children, and so on. In contrast, an Iroquois-type organisation distinguishes cross-cousins from parallel, but there is no co-lexification with spouse and cross-cousin. Iroquois- and Dravidian-style terminologies exemplify the importance of identifying small-scale differences (Godelier, 2012). These types would sit very close to each other in kinspace, due to the predominance of crossness in their organisation - however, the unique of types of crossness should identify them as different clusters.

Detailed study of particular groups sometimes reveal nuanced differences of types resulting in new classifications, such as Australianist's classification of *Kariyarra-type*, mostly found in languages around Australia's Northern Cape York Peninsula and the Western Desert, but rarely outside Australia (McConvell & Hendery, 2017). As with *Dravidian-type*, Kariyarra is a system that is defined through crossness and marriage patterns, but marriage patterns are strictly with one interlocking group, or "restricted exchange". Whether this is a sub-type of *Dravidian*, or a type in its own right is still debated, but it highlights the importance of cultural context and minor structural differences in the classification of kinship terminology.

It is empirically unclear whether we would actually observe the ten clouds predicted by Godelier; typologists often differ on the number of categories they create. It is also unclear whether clouds will contain groups of effectively unrelated languages, as much anthropological

theory predicts, or whether clouds will reflect local variations, as with Kariyarra. However, over time, the anthropological literature has reported a surprising regularity in kinship organisation across unrelated and geographically distant societies (Kroeber, 1909; Murdock, 1949). The literature is yet to offer a solid explanation for why kinship structures can be so similar between societies where we can surmise no, or very little, pre-modern cultural exchange. For example: Swedish (Sweden) and Chipewyan (Canada) have structurally identical organisation in G^0 and G^{+1}, despite being situated on different continents (determined from data in Kinbank). This gives us confidence to predict that clouds of diversity exist, but there is still an onus to observe them.

The conceptual morphological space approach presented in this chapter only incorporates existing knowledge, however, above I have shown how using a new conceptual understanding of diversity can help identify inherent assumptions, and develop new lines of research. The exploration of local variability in kinspace is an idea that is notably under-explored (Godelier, 2012). This should encourage us to explore other sub-spaces of kinship diversity for localised variation, which might reveal similar patterns. In chapter 5, I create a statistical approximation to kinspace. Based on the reasoning in this chapter I hypothesise that the observed clouds should broadly follow existing typological structures (Eskimo-type, Hawaiian-type etc.), and reveal significant patterns of local variation which separate organisations at a more granular level than existing typologies.

4.2.4 Within-type variation

By conceptualising diversity as graded clouds of kinship terminology, we raise an anthropologically interesting question - how similar are the clouds? Similarity in this context can be described in two ways: how similar are languages within a cloud, and how similar are clouds to each other. This section considers the former.

I discussed above that many existing typologies ignore local variation in preference for broader classifying features (Kroeber, 1909; Murdock, 1949). To some degree this is the goal of the typology - to provide useful categorical features for analytical gain, but in doing so, it constrains us from understanding within-type variation. For example, a typical Hawaiian-style organisation uses sibling terms for all first cousins, but there is considerable variation in how this is enacted. In the Pacific, and typical of Tongan, siblings and cousins are referred to in terms of relative sex (kin terms gloss to meanings like opposite-gender sibling and same-gender sibling). Whereas amongst the Lozi in western Zambia, the Hawaiian-style system refers to cousins and siblings by gender (where terms might gloss as male sibling or female sibling). So, while typologically the same, there are significant differences in how these societies categorise kin. The question raised here, and above, is at what point should localised variation in kinspace be described as a different type? Taking this idea forward, it is also important to ask whether all types equally variable?

In linguistic typology, there is always a tension between the regular and the exception when defining types (Epps, 2010). It is obvious that if a particular kinship terminology structure occurs frequently and independently across the world, then there is evidence to consider this structure as an empirical "type". The case is less clear with low frequency kinship terminology. In general, the answer to defining types depends on the scope of the question. If languages differ on an unimportant dimension (e.g. if two languages are identical, but differ on a single kin type), then they are not different types, if it is important (e.g. distinguishing cross from parallel kin), then they are. However, to make the distinction between important and unimportant dimensions, one must be aware of all dimensions on which languages differ. The need to understand the extent of diversity, before building typology highlights the recent shift in linguistics to pursuing documentation and diversity over broader theoretical reasoning (Evans & Levinson, 2009). Within other linguistic domains (e.g. colour terms), the discovery of universal constraints on diversity stem from a prototypical reference grid from which cross-linguistic comparisons can be made (Evans, 2010). By establishing kinship terminology as a finite domain, we should look to create a prototypical referent to represent this domain. The prototypical referent then provides a platform from which we can extract tractable categories of variation.

The second question I raised above was: Are types equally variable? That is, are some types strictly defined by their structural features, and are other types more flexible? This question can be re-framed in respect to the ordered rules used in OT (section 1.2.2). Recall that a particular terminology is generated using a set of ordered rules, and the order determines the structure of the terminology. In relation to generating a type: Do primary rules influence the likelihood of secondary rules being activated? Or more generally: Do higher ranking rules affect the order or activation of lower ranking rules? This question has been discussed in reference to sibling organisation, where Nerlove and Romney (1967) make five assumptions around how rules might interact:

> "(1) Two relational components will not occur as primary; that is, relative age and same-sex / opposite-sex distinctions will not occur together as primary. (2) If sex of relative is secondary to relative age, it will occur in the elder rather than the younger category. (3) If relative age occurs as a secondary distinction with sex of relative primary, it will be on the male side. (4) If relative age occurs as a secondary distinction, with same-sex/opposite-sex primary, it will be on same-sex side. (5) Sex of speaker may appear as a tertiary distinction"
>
> (Nerlove & Romney, 1967, p. 183).

Nerlove and Romney (1967) use these rules to derive a 12-piece sibling typology, which is the most replicated and stable typology within kinship terminology (Kronenfeld, 1974; Murdock, 1968). Each of these rules have not been empirically explored, but their effectiveness is

explaining observed diversity in sibling terminology offers theoretical integrity to these claims. Of these five rules, the first four indicate the conditional application of rules. Assuming this holds true beyond sibling terminologies, I hypothesise that local diversity is not equal across types, and that within some patterns of organisation there should be more variation than in others. The literature on the conditional interaction of rules is not extensively explored; however, OT seems like a viable framework from which to test whether the conditional interactions expressed by Nerlove and Romney is endemic to sibling terminologies or not.

4.2.5 Temporal forces in Kinspace

Above I discussed how the conceptual space for any particular language can vary over time, but since then we have been considering the space as static - but we know from the phylogenetic testing and transitional models in section 2.3 that terminology changes over time. In this section I explore how kinspace can help understand change in kinship terminology by exploring how distance might work in kinspace, and what that says about terminology change.

In a euclidean space movement is linearly constrained. That is, with three points in a line, it is not possible to go from the first point to the last point, without going through the second. This logic also extends to predictions of similarity, assuming the three points are equidistant, the middle point should be the average of the two terminal points (Mitteroecker & Huttegger, 2009). The constraints imposed within a spatial understanding of similarity raise the question: Does constrained change also occur within kinship terminology?

Early studies of kinship terminology evolution theorised unilineal models of change, but these theories have been largely discredited for using ethnocentric and incorrect models of evolution (e.g. Morgan, 1871). Modern views of terminological evolution are more flexible than their early counterparts, offering multiple routes for change, and highlighting that not all change is equally likely to occur (Tjon Sie Fat, 2018; Viveiros de Castro, 1998). However, many of these models assume system wide change, where recent research suggests that kinship systems may change in a more modular pattern (Rácz, Passmore, Sheard, & Jordan, 2019). This modular approach is also in line with an external hypothesis of change, suggesting that different social structures influence different terminological modules (e.g. cousin organisation and marriage patterns; Parkin, 1997). My contribution is to propose a new approach for looking at change using OT and suggest that random drift through this model might explain some amount of variation in kinship terminology diversity.

First, I briefly address whether kinspace is euclidean. The simple answer is no, but to answer how the space is structured is complex. In a euclidean space a position that is equidistant from two other positions is by definition the average of the two positions, and importantly, they can only have one average because the space in linear. In terms of kinspace, average similarity could come from a number of different terminological organisations. Taking a simple example of three kin types: A, B and C. These can be organised five different ways: one term for all types, one

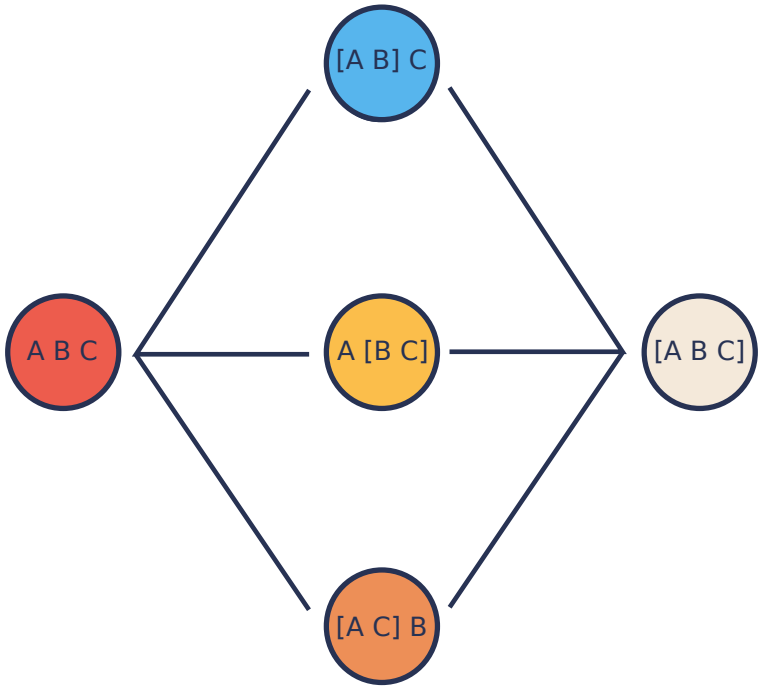


Figure 4.4: A display of distance in kinspace as non-euclidean. Kin types (A, B, or C) are grouped with "[]", in five possible ways. The terminology points in the middle are "averages" of the terminology on the left and right, but since there is not a single average, the space cannot be euclidean.

term for each type, and three ways of grouping the three types under two terms. Taking the single term as the start point, and the three unique terms as an end, we could consider each of three two-termed organisations as equidistant. They are therefore averages in a conceptual, but not in a numerical, sense (figure 4.4). This is a purely structural view of the problem, and theoretically kinspace also varies on dimensions of sound (Are Spanish sibling words, *hermano* for brother and *hermana* for sister, considered more or less similar to English sibling words?), or semantics (Do the French terms *cousin* and *cousine*, prescribe different behaviours or are they semantically identical?). How these extra dimensions might interact with similarity are not well explored in the kinship literature, so how they might influence kinspace structure is unclear, but it is unlikely they would result in a euclidean kinship space.

To build a model of constrained change in kinship terminology, I utilise an OT framework to identify likely patterns of change. Existing models have been proposed for sibling typology (e.g. Epling et al., 1973), from which I will base a model on here. Epling et al. derived a network change for sibling terminology using binary partitions as links between types. The English system [B Z] can transition to an [eB yB Z] organisation through the binary partition of the brother term. Equally, complete partitions would see [B Z] move to [eB yB eZ yZ]. Here, I deviate from this model by including weighted change as described by OT. Using OT, the the likelihood of a change is weighted by the order of OT rules - the lower ranking the rule,

the more likely it is to change. For example, in English, introducing gendered cousin terms is considered a smaller change in OT rule order, than the introduction of a gender of speaker rule. By using a weighted rules change all changes are possible, but due to the weighting, many changes will be very unlikely.

The links between possible organisations creates a network of possible change in kinship organisation, where nodes are plausible organisations, and edges are the rule changes weighted by their likelihood of change. In addition to the OT weighted rules, cognitive and psychological research has suggested that relational rules are not only more difficult to learn than conjunctive rules, they often are learnt later in development than other concrete objects (Gentner & Loewenstein, 2002). Relational constraints are determined relative to an attribute (e.g. age relative to ego), and conjunctive constraints are a single attribute (e.g. gender) - this is particularly the case in children (Bruner, 1986; Ciborowski & Cole, 1972). Finally, I expect that complete rule changes, as with complete partitions, are less likely to occur than their partial counterparts. For example, extending the sibling example above, we might expect that the addition of relative age to *brother*, which requires at minimum one additional term, is more likely to occur than the complete partition of relative age in all siblings, which requires a minimum of two new terms. This is an extension of the idea of minimal change, in that a partial change will result in less new terms than a complete change. However, there is no experimental evidence which has tested this assumption.

Whether complete or partial rule changes are more likely is a point for debate. Here, the difficulty in creating new words is considered the primary constraint on why partial changes are more likely. Rule based approaches might argue that complete changes are more likely to occur because they create more cogent categories than partial changes (Read, 2013). As far as I am aware, there is no empirical research exploring which of these possibilities is more likely. However, there many ways a language can adapt when adding a new term: morphological modification of an existing kin term to cover a new category, borrowing a term from another domain, loaning a kin term from another language, amongst others (Allen, 1989). When reducing the number of kin categories, similar changes can occur depending on whether the new category extends an existing one, or requires a new label (Allen, 1989). Each of these emphasise the adoption or creation of a single term to mitigate a terminological change, rather than new categorisations, and therefore rely on this logic that partial changes are more likely, with the knowledge that this logic may need to be revisited.

In this instance, networks are a more useful tool to convey ideas of change than kinspace. However, we can consider the networks in terms of kinspace. Imagining a topography of kinship space over time, we should observe languages moving through channels of variation between typological clouds. The network then is representative of the channels between clouds, where languages within the channels are likely moving between stable organisations. A common anthropological problem that we are encountering here, is that any observation of a society

is a snapshot in time - it could be a snapshot from a stable part of history, or in the midst of extreme change. While we can imagine languages between channels as transitional, it is ultimately impossible for us to know how long languages that sit between two organisations will remain that way. We have so far assumed that languages always follow the channels of change based on our network, but for any particular language we might observe deviations from these channels due to external forces (such as migration or uptake of a new religion). The model we are proposing could be expanded to deal with these forces, however, currently assumes unobstructed change.

4.3 Conclusion

In this chapter, I have explored the literature behind kinship terminological diversity by conceptualising diversity in kinspace. By using a spatial approach, I establish a prototypical referent in order fully appreciate the breadth of diversity in kinship terminology. The finite set of kinship terminology opens analytical avenues and to establish a topographical and temporal understanding of kinspace. Using these tools we generated hypotheses about observed kinship diversity - which explicitly are:

1. Global diversity should show clustering, which could be used to determine a kinship typology.
2. Within-type diversity is not equal across types.
3. Kinship terminology drift is constrained by minimal change.

This chapter has aimed to summarise the literature and generate hypotheses under a morphological framework. We can progress the field further by testing these hypotheses and concepts empirically. In chapter 5, I attempt to approximate kinspace by quantifying the structure of kinship terminologies and calculating their similarity. By calculating similarity between languages, I create an N-dimensional space which can project into an observable space (using dimensionality-reduction techniques) and then identify common clusters of kinship terminologies. Using this conceptual approach to diversity in combination with a new quantitative procedure, we hope to combine the existing theoretical understanding of kinship typology with the data-driven methodologies increasingly popular in interdisciplinary research.

CHAPTER 5

A quantitative approach to Kinspace

5.1 Kinship terminology and structure

Chapter 2 and chapter 4 both conclude that the six-piece typology (described in box 1.1) fails to accurately represent diversity and is not universally predictive of other aspects of society (e.g. marriage, descent, or residence). In chapter 2, I showed that the existing six-piece typology is not predictive of social structure patterns though phylogenetic and co-evolutionary analysis, concluding that this may be due to the coarseness of the typology categories. In chapter 4, I discussed how many kinship specialists acknowledge the failings of the six-piece typology as a categorical tool, highlight the contemporary literature on kinship diversity, and re-conceptualise these ideas within a morphospatial approach, named kinspace. Kinspace highlights that, although the patterns in the typology are observed, the "broad-brush" categories mask considerable within-type diversity, which is important to consider when understanding the relationship between languages and social structure. By design, typologies should mask some amount of diversity in order to emphasises patterns of interest and minimise noise. However, anthropological interests have shifted to an interest in understanding diversity and variability (Evans & Levinson, 2009). The shift of theoretical interest means the existing typology no longer emphasises patterns of analytical value and is in need of re-evaluation. This chapter will estimate kinspace using a combination of dimensionality reduction techniques and density-based clustering in order to propose a new and improved kinship terminology typology.

The six-piece typology has been disregarded for the most part by kinship specialists (Kronenfeld, 2006), but is still relied upon fields of evolutionary anthropology (Cronk et al., 2018) or economics (Enke, 2019). Possibly, this is because the typology is still used as an introductory tool to cultural diversity and kinship (e.g. Stone, 2014). The primary critique of this typology is that it does not sufficiently represent contemporary knowledge of kinship terminology diver-

sity. While the goal of kinship theorists has always been to understand how the omnipresence of kinship terminology interacts with constructions of society, the collective understanding of evolutionary theory and an increasing depth of ethnographic knowledge has seen the field focus on the details and diversity of terminology structure, rather than hunting for universal laws of terminology (Godelier et al., 1998).

It is also important to note that a typology is only a summary of the data available to date (Song, 2018). Since the development of the existing typology, there has been a significant development in theoretical understanding of kinship terminology (Godelier, 2012) and an increase in availability of depth of the ethnographic record (e.g. the electronic Human Relations Area Files, hraf.yale.edu). The existing six-piece typology has failed to facilitate this evolving theoretical direction, and many ideas resulting from its categorisation have been discredited (See chapter 2; Kronenfeld, 2006). In light of contrary ethnographic examples and new knowledge on the breadth of diversity, it is clear that the existing typology needs updating. As interdisciplinary scientists increasingly rely on these assumptions to infer patterns of behaviour in cultural groups (Cronk et al., 2018; Enke, 2019; Schulz et al., 2019), kinship theorists need to develop a united front in what conclusions can be drawn from the relationship between kinship terminology and behaviour.

Typologies are a useful way to present a fields understanding of diversity. As briefly mentioned in section 4.2.4, the goal of a typology is divide the diversity into tractable categories suitable for more interesting analysis to build from (Song, 2018). Typologies in themselves are descriptive and tell us little about the history and development of whatever domain that they are applied in. It is the analysis that can build on typology that reveals the interesting patterns of human history, and for these analysis to be reliable, so too must the typology be. However, without establishing the distribution of observed diversity, we cannot be sure whether the existing typology is dividing diversity "at the elbows", or is only creating theoretically pleasing divisions (Evans & Levinson, 2009). The existing top-down approach to typology inherently ignores the complexities of observed diversity in favour of theoretical consistency, leading for calls of a bottom-up typological rethink (Kronenfeld, 2006).

Here, I heed the call and build a typology from the bottom up, using observed kinship terminologies sampled from the kinship terminology database, Kinbank (chapter 3), and a computational approach to analysing kinship terminology structure. The analytical pipeline converts terminologies into dichotomised structural vectors. With a numerical representation of a kinship terminology I build a multi-dimensional space representing kinship diversity, *kinspace* (conceptually discussed in chapter 4). Briefly, kinspace involves projecting kinship diversity into an observable space from which to identify regular structures in kinship terminology. I analyse kinspace using density-based clustering methods to automatically identify clusters of similar organisations (McInnes, Healy, & Astels, 2017), and project kinspace into two-dimensional space using dimensionality reduction techniques (McInnes, Healy, & Melville, 2018). Using

these tools alongside the conclusions drawn in section 4.3, I propose two hypotheses:

1. Kinspace will reveal clusters of kinship terminology, which can inform typology.
2. Kinspace clusters will not be equally variable

I interpret the resulting categories of kinship organisation using an Optimality theory framework (OT, see section 1.2.2), from which I build a network of likely change (Jones, 2010). I then show that the derived OT network predicts the global diversity of sibling and grandparental terminology, but not other parts of kinship organisation, suggesting kinship systems change in modular ways, and are subject to different internal and external pressures (Rácz, Passmore, Sheard, & Jordan, 2019, and as proposed in section 4.2.5).

This chapter will proceed as follows: first, I discuss the data used in the analysis. Second, I describe the process of making structural vectors of kinship terminologies, and the pipeline to identifying clusters, followed by the limitations and analytical choices made through this process. Third, I present the results of clusters, discuss how these relate to existing typologies, and how a quantitative approach to typology may improve or replace existing models, and how clusters relate to each other across different kin type subsets. Finally, I look at the structure of kinspace, propose a model of change, and show how that model of cognitive drift constrains diversity.

5.2 Data

The data used in this paper is drawn from Kinbank (chapter 3). Kinbank contains kinship terms for a global sample of 1,151 languages, with focused sampling on large language families that are linked to existing anthropological databases (e.g. D-PLACE; K. R. Kirby et al. (2016)) or dated linguistic phylogenies (e.g. Gray et al., 2009). The most sampled languages families are Austronesian (375), Atlantic-Congo (117), Indo-European (105), and Pama-Nyungan (104). The database contains a core set of 100 kin types each of which has an affiliated kin term. Kin types are derived from a genealogical grid of relationships spanning from grandparents to grandchildren, and between parent's siblings, and parent's siblings' children, with an additional set of affinal kin types (although I do not use affinal terms here). The database contains distinctions for relative age, gender of speaker, and relative age of connecting relative (where appropriate).

5.3 Quantitatively representing structure

In any computational approach to language, the primary difficulty is representing a list of words in a numerical way amenable to statistical methods. Previous attempts at quantifying kinship terminologies from the language-level data have used lower level type-categorisation to

assess linguistic alignment with social structure (e.g. does the language use unique grandparent terms, have two terms, or one term; Whiting et al., 1988), or analysed subset of terminologies using rule-based features for analysis (e.g. does a language distinguish relative age; Jordan, 2011).

Here, I convert the structural patterning of kin terms within a language into what I described as a structural vector. A structural vector is a numerical representation of a particular languages' kinship terminology using binary, pairwise comparisons (see figure 5.1 for a diagram of the pipeline). A structural vector is built by comparing each kin type (category of kin) to each other and signalling whether they have the same (1) or different (0) kin term (the word used for a category), where each comparison is considered a feature of that terminology. Using English as an example: the kin types: mother's brother and father's brother are both referred to using the kin term *uncle*, which means when these terms are compared they coded as 1, however when mother's brother is compared with the kin type father, the feature would be coded as 0, since the kin terms would be *uncle* and *father* respectively. By using binary comparisons, the structural vector only the structural categorisation of kin, and makes no inferences on the morphological similarity between words within a terminology.

There are two complications to this process: 1) some languages have multiple words for the same kin type, 2) binary comparisons mask variation that might be informative. The current process currently assumes a single term for each position in the genealogical grid. In the case where are there are multiple terms, a term is chosen at random. This could potentially decrease similarity between languages by changing the similarity of particular features. An alternative approach is to ask if *any* kin terms match between genealogical positions. Comparing this approach to the approach used yielding structural vectors that were the same in 99% of cases, which suggests multiple kin terms are uncommon. Secondly, by making a binary comparison between terms (same or not) we remove some information that might be informative. For example: the current set up would treat English sibling terms (brother, sister) the same as Spanish sibling terms (hermano, hermana). Using a word distance technique would accommodate this difference, however, this approach contained too much noise to detect any discernible patterns, so the variation was scaled back to binary comparisons.

The structural vector is the result of all kin types being compared to each other once (direction of comparison is not important). Repeating the process for all available languages results in a matrix where each row holds a structural vector of a particular language, and each column represents a comparison of kin-types, which will be described as a feature. The distance between any pair of rows in the matrix represents the structural similarity between those languages (distance metrics are discussed below). The structural vector is an exhaustive description of the structural elements of a kinship terminology and allows us to avoid imposing *a priori* assumptions on which features are important. Existing approaches to exploring kinship diversity impose restrictions on kinship diversity, whether that be for theoretical or computa-

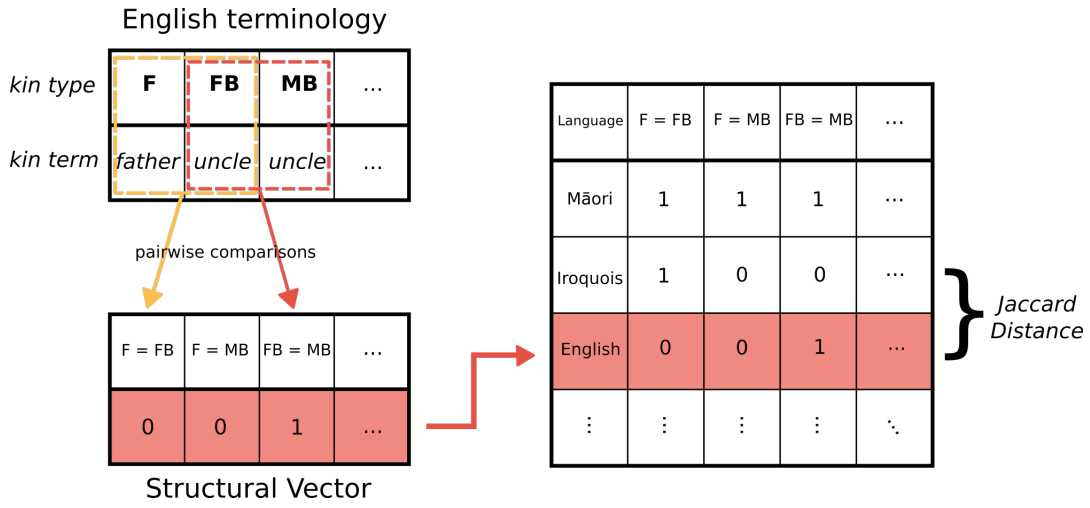


Figure 5.1: Diagram showing the creation of the structural vector. Starting with a list of kin types and kin terms for a particular language, kin types are compared pairwise, asking whether they have the same (1) or different (0) kin terms. This process creates the structural vector. Completing the process for all language gives us a matrix of structural vectors. Jaccard distance determines the structural distance between any two societies.

tional reasons, but by using the approach described here, the diversity in kinship terminology can be observed directly.

Jaccard distance is used to measure the similarity of structural vectors. Jaccard similarity is defined as the number co-existing features, divided by the total number of features. To convert Jaccard similarity to a distance, the score is subtracted from 1. A score of 0 would indicate two languages have identical structure (e.g. two languages that have gendered sibling terms), and a score of 1 indicates there are no overlapping features (e.g. a language with one term for all kin compared to a language with unique terms for all kin). Jaccard distance is defined as:

$$d_j(A,B) = 1 - \frac{|A \cap B|}{|A| + |B| - |A \cap B|}$$

Notably, Jaccard distance excludes similarities where both languages do not have a feature (i.e. both languages indicate 0 for a particular comparison). As discussed in chapter 4, there are many features that, for reasons of cognitive efficiency, are unlikely to occur (Kemp & Regier, 2012). For example, it is unlikely that a kin term would be used to refer to *father's elder brother* and *mother's younger sister's daughter* and no one else. Since many features are unlikely to be present, structural vectors will often be sparsely populated, particularly as dimensionality increases. Because of this sparseness, it is sensible to use a metric which emphasises co-existing features between languages and ignores comparisons that are likely to be uninformative (in this case, because the feature is absent for all or most languages). Including mutually absent features in the similarity calculations will inflate the similarity scores and structures considered to be conceptually different will be numerically similar.

Calculating Jaccard distance pairwise between all languages results in an $N \times N$ matrix of similarity (where N is the number of languages). In order to visualise the distance matrix, I use a dimensionality reduction technique called Uniform Manifold Approximation and Projection (UMAP) to project the distance matrix into two-dimensional space (McInnes et al., 2018). The UMAP projection allows us to visualise kinspace and whether we observe clusters of kinship terminology (hypothesis 1) and whether the clusters are equally variable (hypothesis 2). If there are regular structures in kinship terminology, we should observe clusters of languages within the UMAP projection, and if not, random scatter.

To determine whether the clusters observed in UMAP are statistically separate, and further the exploration of hypothesis 1, I use hierarchical density-based clustering (HDBSCAN; McInnes et al., 2017). Density-based clustering detects clusters based on the density of points (here: languages), rather than the distance of points from a centroid or other metric (as in other cluster approaches such as k-means). Functionally, using a density-based approach means that the shape of clusters does not need to conform to any shape or probability distribution, so long as they maintain the required level of density. This benefits us as existing kinship theory suggests that within-type diversity is not equal, meaning clusters of languages are not likely to all conform to the same shape (discussed in detail in chapter 4.2.4). A second benefit of using a density metric, is that the approach can automatically detect the number of clusters and outliers without human specification. By using approaches with minimal specification, the number of *a priori* assumptions are further reduced and we can determine whether the existing typologies occur naturally in the data, while also not forcing the categorisation of languages which have diverged from expected patterns.

For all bar one parameter in the HDBSCAN algorithm I choose the value that minimises outliers (for details see Appendix C, table S5.1). The one parameter that must be set is minimum cluster size, which poses an interesting anthropological question - how many languages are needed for a type to exist? In linguistics, a type is defined as a category which contains a plurality of characteristics, but the requirements to observe a type are often left vague (Greenberg, 1973). For example, Greenberg suggests that when numerically analysing a linguistic phenomena, any clustering of languages around a mode would indicate a typical type. However, under a theoretical approach, all types that can be theoretically proposed can exist regardless of their frequency (or existence). However, this approach has led to theoretically predicted but unobserved types, which might question the viability of the theoretical approach (e.g. Allen, 2009). A considerable debate could be had on whether a type can be determined by frequency or whether it only needs to be explained by theoretical framework - but to progress this analysis a figure is needed. I conservatively chose 10 languages.

At the end of the analytical pipeline two outputs are created: the projection of kinship diversity into two-dimensional space and the statistical identification of terminology clusters. These outputs allow us to review kinship terminology diversity within kinspace, identify where

divisions exist (hypothesis 1), and whether these divisions are equally variable (hypothesis 2). Section 5.6 looks at the output of the analytical pipeline for a number of kinship terminology subsets and looks to provide quantitative answers to the two hypotheses.

A secondary benefit of this similarity approach allows the use of distance between clusters to build theories of terminological change. As distance between languages is representative of similarity, so too is the distance between clusters. Using a cluster as a typological representative, and inferring a typical terminology for each cluster, distance between types in kinspace might be indicative of typological change. This is discussed in more detail in section 5.8.

Throughout the analytical process, I am required to make some assumptions and analytical choices - as with any quantitative approach. The next section discusses these choices and describe what has been done to minimise their influence and how these decisions influence the interpretation of results.

5.4 Data limitations

In this chapter, I am interested in observing the breadth of observed diversity in order to determine whether there is a convergence of terminology structure across the globe. Here, I am specifically analysing structural diversity. While linguistic diversity encompasses a much broader range (semantic similarity, syntactics etc.), the structure of kinship terminology is traditionally thought to reflect the structural norms of society, which has been the primary goal of kinship terminology typology (Murdock, 1949). The identification of terminological clusters will help inform a new kinship typology that would be predictive of social structural differences.

Since the Kinbank database is structured upon a grid of genealogical relatedness, with additional divisions for relatives age (e.g. elder or younger brother), relative gender (e.g. same or opposite gender siblings), and age of connecting relative (e.g. mother's elder sister's daughter) extracting the structural vector for each language is a straightforward computational task. Kin terms are connected to genealogical relationships, and the terms used for all genealogical relationship are compared to create the structural vector. Kinbank has the potential to explore some other aspects of similarity (e.g. phonological and morphological) but these are avenues for future research.

More importantly to the database, transcribing structure of a kinship terminology is an objective task, as opposed to the subjectivity of the semantic meaning of kin terms. In the ethnographic record, it is relatively common for kinship terminology to be recorded against a genealogical grid, or at least using English descriptions of the categories. The use of an etic grid within an ethnography aligns with the organisation of Kinbank and makes the collation of data a transcription task. The semantic coding of kinship terms, on the other hand, requires an emic understanding of society. An internal and functional description of kinship terminology

is ultimately subjective description of kinship terminology. Anthropologists aim to minimise their own experiences in the understanding of other societies, but it is difficult to parse macro-level processes in the linguistic categorisation of kin from any individuals' personal experiences, whether that be from the interviewee or interviewer. The problems facing a semantic analysis of kinship terminologies at this scale are not insurmountable. To do so one could develop a systematic toolkit for anthropologists to use in order to have comparable representations of semantic structure and to have this deployed at various sites. However, this would ignore the large existing literature of anthropological research and may be more appropriate for a separate project.

5.5 Analytical decisions

Through the pipeline described in section 5.3 I develop a statistical approximation of structural kinship diversity space. However, there are a number of practical problems, deriving from computational limits, that cannot be overcome. In the following paragraphs I discuss these problems, what their impact on our understanding will be and how the impact is minimised.

The most far-reaching concession this quantitative approach requires is a limit on dimensionality (i.e. a limit to the number of features). We are limited in the number of dimensions we can analyse in two ways:

1. The number of dimensions that are computationally manageable is lower than the number of dimensions that theoretically exist, and

2. Only languages with which we have a complete set of kinship terms can be analysed.

The first problem has been faced by other typologists, whose solution was to divide terminologies up into smaller sections (e.g. siblings, cousins, uncles, aunts, etc.; Jones, 2003a; Murdock, 1970). I follow in the footsteps of these papers, although with increased computational power, larger subsets can be used and here I analyse kin type subsets by generation, rather than the more common division of generation and gender (e.g. Jones, 2003a). Consequentially, I discuss results in the following subsets: sibling terms (as a proof of concept), G^0, G^{+1}, G^{+2}, and G^{-1}. Recent research has suggested that the strength of co-selection between generations is weaker than previously thought (Passmore et al., In preparation). In an unpublished manuscript, and in collaboration with colleagues at ANU, we used Kinbank to show that the typological categorisation of G^0 was moderately correlated with the typological categorisation of G^{+1}. Further exploration found this effect was mostly driven by a strong internal coherence present in *Eskimo-type* languages, but the strength of this relationship was not found between generations in other terminology types (Passmore et al., In preparation). The suggestion of modular (or generational) changes in kinship terminology evidence offers support for the divisions made in the past and in the analysis performed here. However, sub-setting the data by

generation means we do not incorporate patterns of generational skewing (when kin terms are used across generations), meaning we will not be able to detect types such as *Crow-type* or *Omaha-type*. Since these are identified in the six-piece typology, this is a disappointing drawback. Analysing generational subsets (i.e. sub-setting kin terms by lineage) would circumvent this problem, but since these types each only make up 9% of observed variation we omit them from this analysis.

Additionally, Kinbank contains distinctions based on relative age, relative gender, and age of connecting relative. Incorporating all these possible distinctions will increase dimensionality to an unmanageable level. To determine how much impact the exclusion of these rules might be, I use descriptive statistics to see how often these rules are invoked. If they do not occur frequently, then they are set aside - the extent to which this effects each subset is discussed in their respective results sections below.

Within G^0 and G^{+1} it is necessary to reduce the subspace further since dimensionality is too high for HDBSCAN to work effectively (McInnes et al., 2017). Potentially, the kin type subsets could be divided further (e.g. analyse cousins separate from siblings), however I opt to using the top 100 predictive features using a random forest and then perform the space approximation and clustering using only these features (as recommended by Pedregosa et al., 2011). While we ideally would incorporate all features, we have already established that many comparisons of kin types are not going to be informative. Using this approach allows us to remove uninformative features and maintain a consistent pipeline of analysis throughout.

The second constraint is that we can only analyse languages with lexical data for each of the considered kin types. The need for complete data is somewhat mitigated by the previous constraint, analysing genealogical close kin. Genealogically close kin are cross-culturally more likely to have kin terms, thus minimising the likelihood that any particular language would have missing kin terms. However, the data used is also constrained by both the ethnographic literature and practical decisions in the creation of Kinbank. The ethnographic kinship literature tends to be based on a Eurocentric view of kinship and focuses on describing relationships within the domains of European kinship (i.e. parent's siblings and their children, and grandparents to grandchildren). Some societies may have terms for three generations (or more) above or below ego, however, the constraints on lifespan and reproduction mean that the number of societies who consider kin beyond these generations are few and most societies would only have three concurrent generations (Fenner, 2005). Where we might under represent diversity, however, is when the definition of kin extends beyond second cousins or is restricted within parent's siblings. Some kinship theorists argue an extensionist view of kinship, where terms are extended from closer to more distant relatives (Shapiro, 2008, although this is debated see Parkin (2012) for a summary). In the case where kin extend beyond the types captured by Kinbank, we should still capture some part of the principle that determine the extension (e.g. if Hawaiian-style cousin organisation extends to second cousins, the extension relationship will

be detected in the connection between siblings and parent's siblings' children). Unfortunately, the requirement of complete sets means languages must be excluded when terms are more constrained that our kin term subsets. For example, Altaic languages of Mongolia do not have terms for paternal cross-cousins, which would exclude them from the analysis of G^0 (Krader, 1953). It is worth noting that this is not a restriction of the pipeline discussed here, but of quantitative approaches more generally.

The third concession is not controlling for phylogenetic relationships between languages when clustering. Briefly discussed in section 2.1.1, two languages that are closely related, because the both descend from a common language, or have recently borrowed a number of linguistic or social features from each other, are more likely to be similar than two languages who have a distant historical relationship, or little contact. The interdependence between languages, or auto-correlation, means that particular terminology structures may be over-represented if we sample too heavily from a particular language family or geographical area. Auto-correlation amongst languages present two analytical problems: 1) there is not currently a single language phylogeny that would incorporate the relationships between all (or even half) the languages in the sample, and 2) there are no clustering methods that would account for phylogeny in the appropriate way. Ideally, the clustering method would control for phylogeny by interacting with the minimum number of clusters parameter, allowing the model to scale the minimum cluster size parameter to distinguish between a cluster of 10 closely related languages and a cluster of 10 distantly related languages. I have attempted to mitigate the impact of auto-correlation *post-hoc* by including a measure of diversity in the descriptive cluster statistics, discussed more below. Currently, however, I am not of aware of any methods which would allow for relatedness in clustering to be accounted for *a-priori*.

The final analytical decisions I make is to only analyse observed diversity, and not theoretically possible organisations. I choose to analyse observed diversity here because I want to focus on identifying clusters of observed kinship diversity, from which to build a typology. Another way to approach the analysis of diversity is to simulate the structural vectors of all possible organisations, and determine of those, which are observed, and which are not in order to identify subsets of kinship terminological space.

To summarise the preceding sections: we have provided detailed description of our analytical pipeline, moving from the raw data to structural vectors, establishing an approximation of kinship space using the vectors and UMAP, and clustering the vectors using HDBSCAN. There are some assumptions we have needed to make in converting the linguistic domain to a numerical vector, however, these assumptions are either justified, their impact is minimised, or I have identified their impact if they are not. In the following sections we discuss the results of the analysis for each subset of kin terms.

5.6 Observations in kinspace

The following sections describe the UMAP projection and HDBSCAN clustering for each subset of kin types. In each subsection I describe the input data, identifiable clusters, and the UMAP approximation of structural kinship space. The identifiable clusters are presented in a table describing the types they represent, with frequency and diversity scores (Inverse Simpson's index) of those types, followed by a silhouette score indicating the density of the cluster. The inverse Simpson's index and silhouette scores are defined as:

> *Inverse Simpson's Index:* The probability that any two languages with the same cluster come from different language families (Morris et al., 2014).
>
> *Silhouette score:* The average distance of languages within a cluster to the neighbouring cluster, varying between -1 and +1. +1 indicates all languages belong in their allocated cluster, zero indicates some languages may belong in other clusters, and -1 indicates all languages belong in the neighbouring cluster and this cluster is ill-defined. (Rousseeuw, 1987).

I present counts and diversity scores to account for the possibility that some types may be over-represented due to shared ancestry or borrowing within a language's family. Silhouette scores are a post-hoc test used to determine whether derived clusters are statistically separable. There is no independent scale of silhouette scores from which we can determine the strength of clustering, but recent cross-cultural research found an average silhouette score of 0.18 (Miranda & Freeman, 2020).

Additionally, each subset is presented with a UMAP approximation of kinspace. In these figures, each point indicates a language, and points are coloured to reflect different clusters identified through HDBSCAN. Within each cluster is a letter linking the cluster to the descriptive table. These graphs indicate relative similarity, so the axis have no interpretable meaning. Distance between pairs of points are meaningful and is indicative of similarity, therefore clusters that are close, are also structurally similar.

5.6.1 Siblings

Sibling organisation is the most replicated typology of kin terms because it is a set of kin that is cross-culturally omnipresent, has a manageable set of semantic distinctions, and is well described in the ethnographic literature (Epling et al., 1973; Kronenfeld, 1974; Murdock, 1968; Nerlove & Romney, 1967). These characteristics make siblings a good subset for testing the viability of the proposed analytical pipeline. There are minor differences between the various papers - so for purposes of comparison, I only reference the Nerlove and Romney (1967) typology (here on N&R).

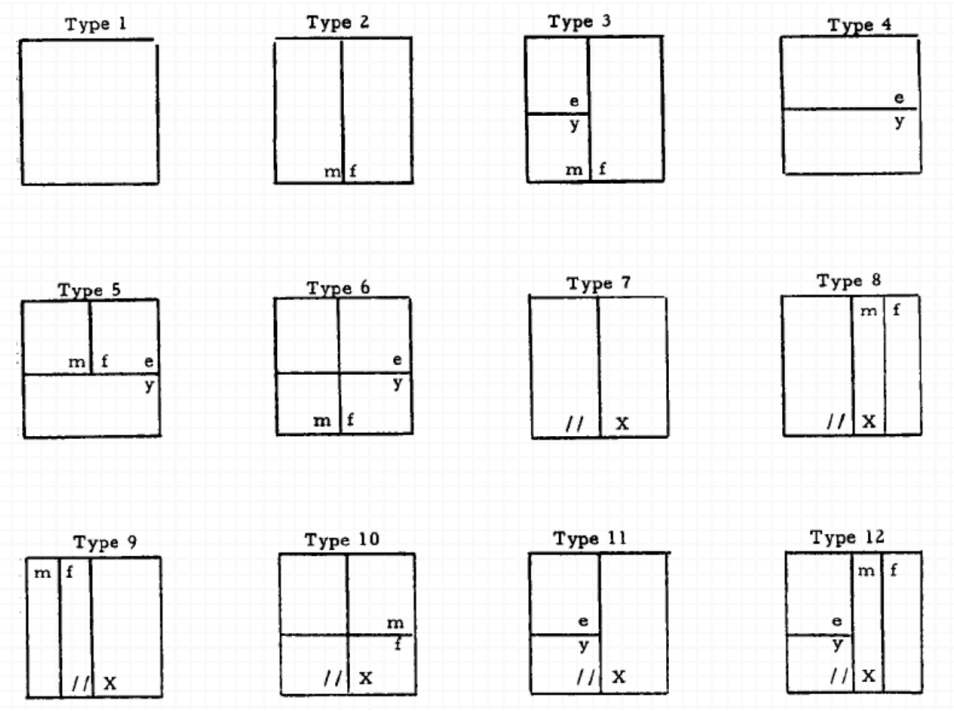


Figure 5.2: Figure 1 from Nerlove and Romney (1967) displaying the bottom-up derived typology. m and f indicate male relative and female sibling respectively. e and y indicate elder and younger sibling. // and X indicate same-gender and opposite-gender sibling. Lines indicate divisions of siblings, and codes are associated with lines. For example: Type two indicates a term for male siblings and a term for female siblings. Type 11 indicates a single term for opposite-gender siblings, and a term for elder same-gender sibling and a term for younger same-gender sibling.

The N&R typology identifies 12 ways to organise eight siblings relationships from 4,140 possible organisations (meB, myB, meZ, myZ, feB, fyB, feZ, fyZ; figure 5.2). The typology is achieved through the layering of rules (e.g. distinguish relative age, distinguish gender), and eliminating disjunctive organisations from the larger set to find this 12 piece typology. This set covers 98% of their 245 language sample as either an identical match, or as derivative types (languages that match a type, but with a single additional rule) or reversed types (mirrored classifications of the type).

The goal of this section is to show my analytical pipeline can accurately identify the existing N&R typology. The accuracy of this comparison will inform how well this approach can be applied to other subsets of kinship terminology. I will also show how the flexibility of density-based approaches improves on the rigidity of the N&R typology, by identifying similar, but not identical organisations.

Within Kinbank, there are 849 languages that contain the eight terms used to establish the sibling typology, which is 75% of the total language sample in Kinbank. There are 85 unique

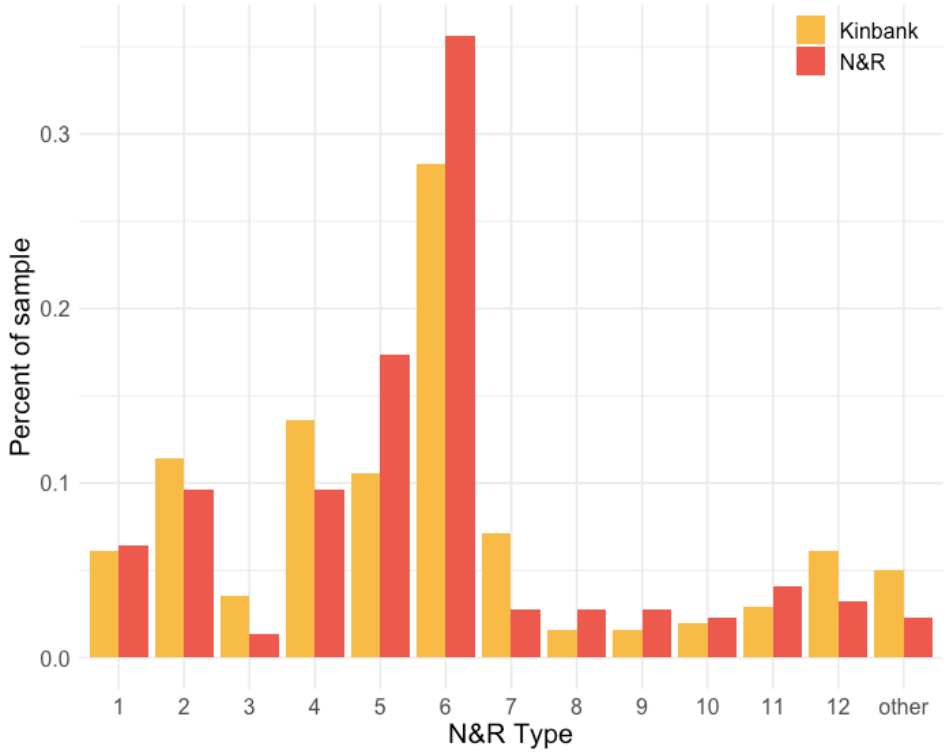


Figure 5.3: Percent of siblings types in total sample from Nerlove and Romney (1967) and the matching percentage in Kinbank. Numbers on the x-axis relate to types in figure 5.2. In general, the frequency of types is very similar between samples.

sibling organisations, identified by the number of unique structural vectors. After applying the HDBSCAN process, 808 of the 849 languages these are classified as one of 15 types, leaving approximately 5% of languages unclassified - slightly higher than the 2% found in N&R. The fifteen types contain all of the N&R typology, two derivative types, and one type that was not previously proposed within existing typologies. The results also find similar frequencies of types that match across the two approaches (figure 5.3).

Table 5.1 reports the description for each of the types identified by the kinspace approach and the corresponding N&R type, as well as their frequency and diversity scores. As is the case for all subsets, clusters are alphabetically labelled in order of frequency (i.e. A is the most frequent cluster, B is the second most frequent, etc.). In the case of siblings, cluster A organisation is the most frequent (212) and is also the most diverse (0.926) - found in 42 of the 73 language families. In comparison, cluster B is the second most frequent type (111) but has a low diversity score (0.517), and only found in 11 language families. Silhouette scores are high for all clusters suggesting clearly defined types in all cases, which is also visualised in the UMAP projection (figure 5.4).

To compare the results from our process to the existing N&R typology, I classify all lan-

guages to one of the 12 N&R types, or as an outlier. Pairing languages to types is performed computationally by creating a structural vector for each of the exemplary N&R types (figure 5.2) and iterating through our observed languages to determine exact matches. I then compare whether the algorithmic clustering matches the N&R categorisation.

Accuracy of clustering is measured using the adjusted rand index. Adjusted rand-index measures the level of agreement between two sets of categories accounting for the chance grouping of languages (i.e. adjusting for group size). The adjusted rand index is calculated twice: firstly, for all languages that we can identify as a N&R type and secondly the entire data set (i.e. including and excluding outliers). When only analysing languages matched to the N&R typology, the adjusted rand index is 1.0, indicating that the kinspace approach perfectly categorises languages that exactly match N&R types. This is a convincing result and gives confidence in applying the kinspace approach to other subsets. However, the power of the kinspace approach is its flexibility to capture similar, but not replicate types. When including languages that cannot be identically matched to the N&R typology, the adjusted rand index is 0.80. Around 5% drop can be accounted for with the introduction of languages which are not categorised through the Kinbank process. Procedural differences make up a further 9% of the difference. The procedural differences are useful discussion points for understanding the benefits and drawbacks of the quantified kinspace approach.

Firstly, since categories are no longer strictly defined, but retain an element of "fuzziness", accuracy will be penalised for including languages that a stricter approach would count as an outlier. To explain, consider N&R type six (figure 5.2) as an example of the graded clustering, which is described by four unique terms: eB, eZ, yB, yZ. N&R type six is represented by cluster A in the kinspace output, but contains 34 languages which do not perfectly match the N&R type (14% of this cluster). The imperfect matches differ on what N&R describe as secondary or tertiary rules and classify as derivative types (table 5.1). The 34 derivative languages tend to have between one to three more terms than the exemplary type six, but still follow the primary rules of the category: *distinguish relative age* and *distinguish gender*. The additional terms often highlight culturally important relationships - for example: Burmese uses a gender of speaker distinction for younger brother, but no other sibling (Brant & Khaing, 1951). The diversity surrounding cluster A is observable in figure 5.4, where a core of identical types highlights the majority of the cluster, but a streak of languages in cluster A are heading up the y-axis (coloured in yellow). It is languages that streak away from the core which are showing primary structural links but differ in secondary or tertiary categorisations. Many of these are captured using our approach (yellow points), but we note that some of these differences are not captured (grey points).

Secondly, N&R classify reversed types under a single category, whereas our analyses will treat them as separate groups. For example: N&R type 3 (eB, yB and Z) includes the reversed, or mirrored organisation (B, eZ, and yZ) as one category - but our approach separates them

Table 5.1: Clustering results for sibling kin types. **Labs.** indicates the identifying character, N is the frequency of occurrence, **Div.** is the Simpson's index diversity score. The diversity score indicates the probability that any two languages with the same cluster come from different language families. **Description** offers a written description of the cluster. **Coded description** is a description using kinship notation. **Silhouette** is the silhouette score for that cluster. Silhouette scores show average distance of languages within a cluster to a neighbouring cluster. A silhouette score of +1 indicates all languages belong in their allocated cluster, zero indicates some languages may belong in other clusters, and -1 indicates all languages belong in the neighbouring cluster. All silhouette scores for the sibling clusters are well-defined, but diversity scores indicates some lineage specific types.

Lab.	**N**	**Div.**	**Description (N&R Type)**	**Coded Description**	**Silhouette**
A	230	0.93	relative age and gender distinctions (Type 6)	eB eZ yB yZ	0.86
B	111	0.52	relative age distinction (Type 4)	(eB eZ)(yB yZ)	0.99
C	93	0.63	gender distinction (Type 2)	(eB yB) (eZ yZ)	1.00
D	86	0.75	gendered elder terms, single younger term (Type 5)	eB eZ (yB yZ)	0.97
E	58	0.37	relative gender distinction (Type 7)	X //	1.00
F	50	0.40	single sibling term (Type 1)	(eB yB eZ yZ)	0.85
G	50	0.42	relative gender and relative age distinction, with gender of speaker distinction in cross terms (Type 12)	e// y// mX fX	0.94
H	29	0.86	Relative age in brothers, single sister term (Type 3)	eB yB (eZ yZ)	0.85
I	24	0.23	relative gender distinction and relative age in parallel terms (Type 11)	X e// y//	0.97
J	16	0.34	gender of speaker and relative gender distinctions (Type 10)	mX fX m// f//	1.00
K	13	0.79	relative age in sisters, single brother term (Type 3 rev.)	(eB yB) eZ yZ	0.70
L	13	0.17	relative gender distinction with gender of speaker for cross-terms (Type 8)	// mX fX	1.00
M	13	0.65	relative gender distinction with gender of speaker parallel terms (Type 9)	X m// f//	0.97
N	12	0.86	single elder siblings' term, gendered younger sibling terms (Type 5 rev.)	(eB eZ) yB yZ	0.93
O	10	0.58	relative gender distinction, with gender of speaker and relative age distinctions in parallel terms (Type 12 der.)	fX mX fe// fy// me// fy//	1.00
-	41	-	Outlier	-	-

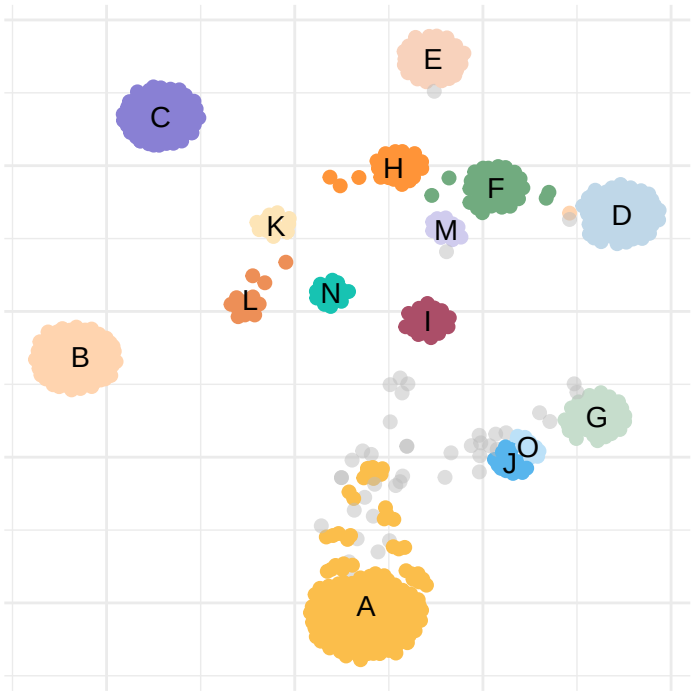


Figure 5.4: UMAP projection of sibling kinspace. Each cluster is labelled with a letter, which links to a row in table 5.1. Size of the cluster is indicative of the number of languages. Siblings organisation shows very tight clusters, however cluster A shows some variability moving up the Y-axis. Grey points indicate unclassified languages.

into cluster H and cluster K (table 5.1). Similar differences occur on three other occasions (all together: between clusters H and K, D and N, and in E and L). While N&R justify categorising these types as one due to their mirrored similarity, I argue that the differentiation of these groups absolutely necessary in understanding kinship terminology variation and the links to social structure, as is discussed in section 4.2.3 surrounding *Dravidian-* and *Iroquois-types*. Accounting for this difference explains a further 5% difference in accuracy.

Finally, the drop in accuracy can also be attributed to the identification of types not in the N&R typology. Since the adjusted rand index is matching the grouping of languages, there is a penalty for having different total numbers of groups. Cluster O is not identified by N&R (nor any other typology), which is described as distinguishing by relative gender, gender of speaker, and relative age. Cluster O is described as impossible by N&R under their first rule: "Two relational components will not occur as primary; that is, relative age and same-gender / opposite-gender distinctions will not occur together as primary", highlighting the importance of continual review of typology in light of new data (Nerlove & Romney, 1967, p. 183). Cluster O is only observed in 10 languages: 5 Tupian languages, 3 Austronesian languages and 1 North Halmahera language, which explains another 1% of changes in accuracy.

This section has shown how the kinspace approach can accurately identify and improve on the divisions from the most replicated typology in kinship studies, while still maintaining a level of flexibility to incorporate more fine-grained differences. Accurately reproducing an existing and replicated typology gives credibility to this approach in identifying the "cultural elbows" of kinship terminology diversity in other subsets of kin types. In the following sections I apply the kinspace approach to G^0, G^{+1}, G^{+2}, and G^{-1} to identify key typological structures.

5.6.2 G^0

Within G^0, or ego's generation, kin types for siblings and parent's sibling's children, accounting for relative age and gender of speaker, are analysed. In total, this is 40 kin types and $\mathbf{1.57 \times 1,035}$ possible organisations. Relative age of connecting relative is another common distinction in G^0. For example: the Indonesian language Kei distinguishes cousins based on relative age, where FeBS is referred to with the kin term *a'an* and FyBS with the kin term *warin* (Guermonprez, 1998). This distinction only occurs in 5% of the languages with no obvious patterning, so it is set aside in this analysis.

503 languages have a complete set of terms for G^0, accounting for 44% of languages in Kinbank, of which there are 259 unique organisations. Clustering reveals 16 types describing 396 languages. The unclassified languages make up 100 of 259 different organisations. The projection of kinspace in figure 5.5 shows more variability than in siblings, which is attributed to the much larger number of combinatorial possibilities in this set of kin terms.

Broadly speaking, there is some evidence for the existing six-piece cousin typology (Murdock, 1949). Due to the subset of kin types used, the only possible types that can be distinguished are: *Eskimo-type, Hawaiian-type, Sudanese-types,* and *Crossed-types* (which incorporate *Iroquois-, Dravidian-, Omaha-* and *Crow-* types). Clusters are labelled accordingly in table 5.2. The clusters identify eight variations of *Eskimo-type*, four variations of *Crossed-type*, three variations of *Hawaiian-type*, and *one Sudanese-type*. Many of the sub-types appear to be lineage specific variations, indicated by low diversity scores, although within each broad category (e.g. *Eskimo-type*) there is high diversity in at least one cluster, suggesting global recurrence. The localised and globalised pattern of diversity is exemplified within Eskimo-types which contain lineage specific patterns of sibling organisation (e.g. cluster F) as well as globalised patterns (cluster O). The mixture of nuclear family distinction with languages family specific patterns of sibling organisation shows how structural differences in terminology can arise at different levels of enquiry, however a more focused analysis would be necessary to determine the importance of these differences.

The identifiability of clusters in G^0 is considerably lower than within siblings, however, is still at an acceptable level in 10 of the 15 clusters, resulting in 10 statistically identifiable clusters in this subset. Five clusters have negative silhouette scores (B, F, G, and M), suggesting these clusters are not statistically differentiated from neighbouring clusters. When calculating

Table 5.2: Clustering results for G^0 kin types. Labs. indicates the identifying number, N is the frequency of occurrence, Div. is the Simpson's index diversity score. Description offers a written description of the cluster, and Glossed description is a reference to the existing cousin typology. Notation is a description using kinship notation. Silh. is the silhouette score for that cluster. Within each Glossed type, there are both global and local variations, highlighting the patterns of local and global diversity in kinship terminology organisation.

Lab.	**N**	**Div.**	**Description (Glossed type)**	**Coded Description**	**Silh.**
A	40	0.30	Relative age sibling terms, single cousin term (Eskimo-type)	eG yG (FBS FZS MBS MZS FBD FZD MBD MZD)	0.34
B	39	0.93	Relative age and gendered sibling terms, single cousin term (Eskimo-type)	eB yB eZ yZ (FBS FZS MBS MZS FBD FZD MBD MZD)	-0.34
C	32	0.82	Cross-parallel distinction (Crossed-type)	B Z (FBS FBD MZD MZD) (FZS FZD MBS MBD)	0.23
D	32	0.81	Unique terms for all relatives (Sudanese-type)	B Z FBS FBD FZS FZD MZS MZD MBS MBD	-0.05
E	31	0.50	Relative gender in sibs & P. cousins, single term for cross cousins (Crossed-type)	X // (FZS FZD MBS MBD)	0.40
F	31	0.19	Single sibling term and single cousin term (Eskimo-type)	(B Z) (FBS FZS MBS MZS FBD FZD MBD MZD)	-0.53
G	31	0.43	Sibling terms, gendered cousin terms (Eskimo-type)	B Z (FBS FZS MBS MZS) (FBD FZD MBD MZD)	-0.23
H	26	0.24	Relative gender distinction (Hawaiian-type)	X //	0.29
I	24	0.85	Relative age distinction across all G^0 (Hawaiian-type)	(eB FBeS FZeS MBeS MZeS) (yB FByS FZyS MByS MZyS) (eZ FBeD FZeD MBeD MZeD) (yZ FByD FZyD MByD MZyD)	0.35
J	21	0.40	Relative gender distinction with relative age, on same-gender siblings (Hawaiian-type)	X e// y//	0.59
K	20	0.76	Sibling terms, single cousin term (Eskimo-type)	B Z (FBS FZS MBS MZS FBD FZD MBD MZD)	0.96
L	17	0.71	Cross cousin, gendered & relative age distinction, parallel groups with siblings (Crossed-type)	(eB FBeS MZeS)(yB FByS MZyS) (eZ FBeD MZeD)(yZ FByD MZyD) (FZS MBS)(FZD MBD)	0.24
M	16	0.65	Relative gender distinction in siblings, single cousin term (Eskimo-type)	X // (FBS FZS MBS MZS FBD FZD MBD MZD)	-0.47
N	15	0.52	Relative age sibling terms, gendered cousin terms (Eskimo-type)	eB yB eZ yB (FBS FZS MBS MZS) (FBD FZD MBD MZD)	0.88
O	11	0.80	Gendered elder siblings, single younger siblings, single cousin term (Eskimo-type)	eB eZ yG (FBS FZS MBS MZS FBD FZD MBD MZD)	1.00
P	10	0.34	Relative gender distinction for parallel cousins, lineal terms for cross cousins (Crossed-type)	X e// y// (FZS FZD MBS MBD)	0.28
-	107	-	Outlier	-	

the silhouette score, the next nearest cluster for each language is recorded, which I use to determine what group languages might be closer to. All negative-silhouette score clusters are *Eskimo-type*, and in all cases the next nearest organisation is another *Eskimo-type* (either cluster K or O). In section 4.2.4, I discussed the likelihood of considerable within-type variability, which these clusters are evidence of. In this case, these sub-types show considerable overlap with other clusters. Further in-depth analysis is necessary to determine why these variants occur and what they might indicate. Cluster D has a silhouette score close to 0 indicating a lot of overlap with other clusters, which may be due to the low frequency of "pure" Sudanese organisation.

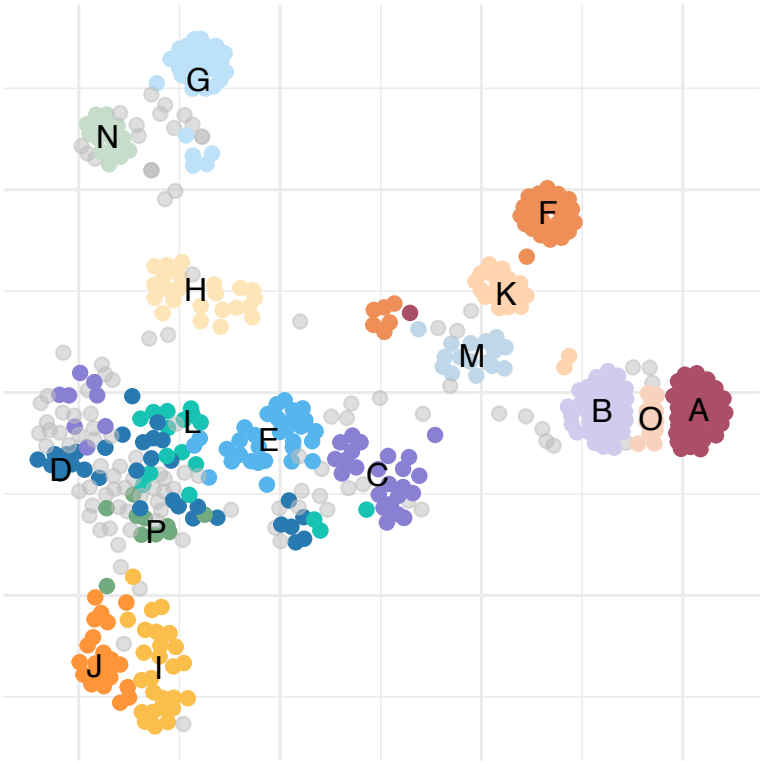


Figure 5.5: UMAP projection of G^0. Here clusters are not as tight and identifiable as in siblings, but 10 clusters are shown to be statistically distinct, as defined by their silhouette scores. The 5 unidentified clusters are B, F, G, and M, which are all part of a broader Eskimo-cluster. All clusters are secondarily close to another Eskimo-type, however, may be marked as unidentifiable due to rogue classifications of nearby and larger clusters. For example: cluster A has a single language identified in another area of the space, moving the centre of that cluster closer to cluster B and impacting the silhouette score.

5.6.3 G^{+1}

The parental generation, G^{+1}, contains parent's and their parent's siblings accounting for relative age (father's older brother vs father's younger brother). Affinal relationships are excluded from this analysis (e.g. mother's sister's husband) because of the increase in dimensionality. However, the analysis of affinal and parent's siblings would be an interesting avenue to explore in future, with many important linguistic and behavioural predictions depending on how these kin types are categorised (Burton-Chellew & Dunbar, 2011; Godelier et al., 1998).

A total of 20 kin types are analysed, which is $5.17 \times 1,013$ possible organisations. In Kinbank, 719 languages contain all these relations (63% of the total sample), with 91 unique types. 12 major clusters are identified, containing 694 of the languages (table 5.3). The 25 outliers make up 22 of the 91 unique organisations. Cluster A, which is the organisation used in English, is the most common (178), but not particularly diverse organisation (0.561) - occurring in 21 language families. The second most common, cluster B (144), is much more diverse (0.913), occurring in

Table 5.3: Clustering results for G^{+1} kin types. Labs. indicates the identifying number, N is the frequency of occurrence, Div. is the Simpson's index diversity score. Description offers a written description of the cluster. Notation is a description using kinship notation. Silh. is the silhouette score for that cluster.

Lab.	**N**	**Div.**	**Description**	**Coded Description**	**Silh.**
A	178	0.56	Parent terms, aunt term uncle term	M F (FB MB) (FZ MZ)	0.92
B	144	0.91	Unique terms for all relatives	M F MB MZ FB FZ	0.91
C	121	0.78	Term for parent & same-gender sibling, unique terms for opp. Gender siblings	(M MZ)(F FB) FZ MB	0.95
D	61	0.78	Unique terms for all relative age relatives	M F MeB MyB MeZ MyZ FeB FyB FeZ FyZ	0.54
E	33	0.56	Special term for MB, otherwise gendered terms	(F FB)(M MZ FZ) MB	0.90
F	31	0.87	Father and FB collapsed, unique terms for all other relatives	(F FB) MB M MZ FZ	0.54
G	30	0.82	Single Aunt term, parent terms, separate uncle terms	(MZ FZ) F M FB MB	0.95
H	26	0.83	Term for mother & her sister, unique terms for all other relatives	(M MZ) FZ F FB MB	0.48
I	20	0.87	Single uncle term, unique parent terms and aunt terms	M F (FB MB) MZ FZ	0.67
J	20	0.10	Gender distinctions	(F FB MB) (M MZ FZ)	0.87
K	16	0.67	Parent terms, relative age parent's sibling terms	M F (FeB MeB)(FyB MyB) (FeZ MeZ)(FyZ MyZ)	0.58
L	14	0.70	Relative age distinction for FB, single terms for all other relatives	F M FeB FyB FZ MB MZ	0.17
-	25	-	Outlier	-	-

31 language families. All silhouette scores suggest that the clusters are identifiable. Cluster L has a relatively low silhouette score compared to other clusters in this subset, and shows large overlap with cluster B. The overlap is not particularly surprising as these organisations only differ in one structural property (relative age distinction in father's brother).

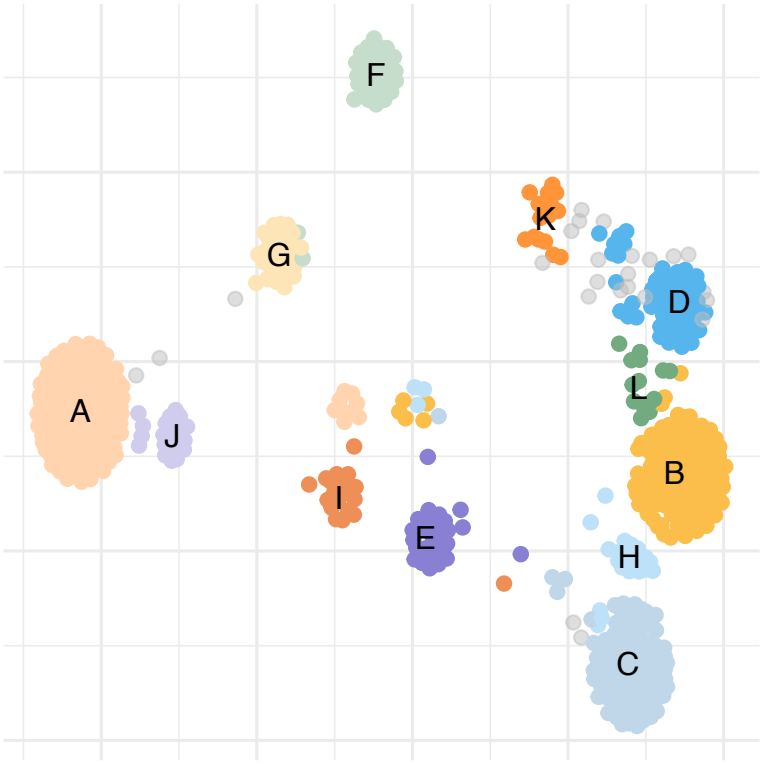


Figure 5.6: UMAP projection of G^{+1} kinspace. Clusters have higher silhouette scores in this subset than in G^{0}, which is reflected in the tightness of clusters in space. There is some variability between clusters K, D, L, and B. The silhouette score for cluster L suggests considerable overlap with cluster B. Clusters B, L, and D are all descriptive or Sudanese style organisation, varying in how widely the relative age rule is applied.

5.6.4 G^{+2}

The grandparental generation contains the four possible grandparents. I analyse grandparental terms for 866 languages (76% of total languages), identifying 13 unique organisations, and 6 identifiable types. 852 languages fit into these 6 types, leaving 1.6% of languages unclassified (table 5.4). This subset has the smallest theoretical space of 15 possible organisations. The two organisation that are not observed are: (MM FF FM) MF and (MM MF FF) FM. That is, the collapse of all grandparental terms, but with a unique term for either mother's father, or for father's mother. These organisations violate the rule of collaterality, which proposes that it is impossible to observe the equivalence of cross-kin, without also making parallel kin equivalent (Héritier, 1981). The rule of collaterality is also present in G^0, where the rule F = MB ≠ FB is never observed. Silhouette scores suggest all clusters are highly identifiable. In G^{+2}, only 1.5% of languages contain a gender of speaker distinction and no common pattern, so this distinction is set aside for this analyses. However, it is important to note that while gender of speaker distinctions are not common organisations, they do exist and are identified as types in other typologies (Murdock, 1970).

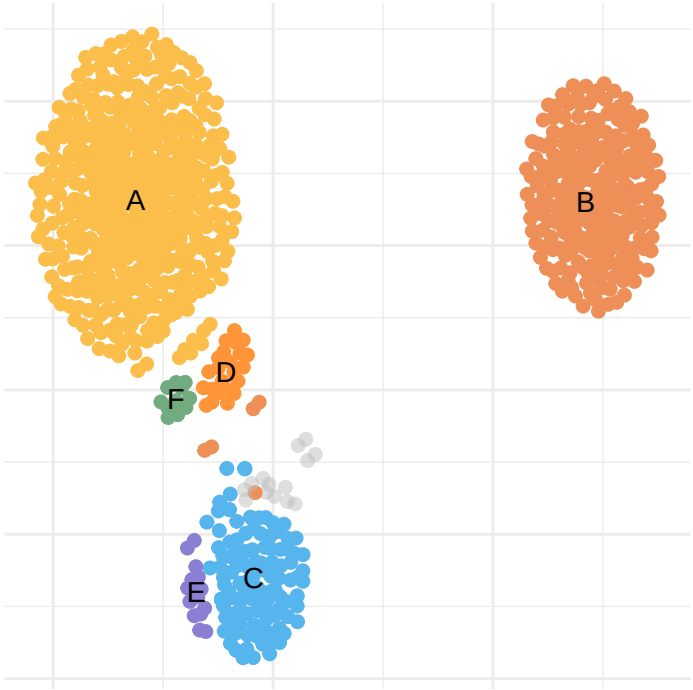


Figure 5.7: UMAP projection of G^{+2}. This subset only identifies six types, although 13 unique types are observed total. Cluster B is considerably distance from all other clusters, which contains a single term for all grandparents. Cluster's A, D, and F all contain at least one gendered grandparent terms. Where as cluster C is completely descriptive (i.e. four grandparent terms), and cluster E contains a lineal grandparent term.

Table 5.4: Clustering results for G^{+2} kin types. Labs. indicates the identifying number, N is the frequency of occurrence, Div. is the Simpson's index diversity score. Description offers a written description of the cluster. Notation is a description using kinship notation. Silh. is the silhouette score for that cluster.

Label	**N**	**Div.**	**Description**	**Coded Description**	**Silh.**
A	466	0.87	Gendered grandparental terms	(FF MF)(FM MM)	1.00
B	233	0.44	Single term for all grandparents	(FF MF FM MM)	0.98
C	105	0.81	Unique terms for all grandparents	FF MF FM MM	1.00
D	23	0.82	Single grandmother term, unique grandfather terms	FF MF (FM MM)	1.00
E	14	0.17	Single term for relative gender grandparent, unique terms otherwise	(FF MM) MF FM	0.91
F	11	0.79	Single grandfather term, unique grandmother terms	(FF MF) FM MM	1.00
-	14	-	Outlier	-	-

5.6.5 G^{-1}

G^{-1} generation contains both children and niblings (sibling's children) with respect to relative age and gender of speaker, creating a set of 20 kin types, and $\mathbf{5.17 \times 1{,}013}$ possible organisations. 600 languages (52% of total languages) hold complete sets of these kin types, with 177 unique organisations across this sample. 16 clusters are identified (Table 5.5), which classify 483 languages. Unclassified languages make up 96 of the 177 unique organisations. Cluster A is the most frequent organisation (102) with moderate levels of diversity (0.802), where terms gloss to son, daughter, sibling's son, sibling's daughter. In figure 5.8 there is a large cluster of uncategorised languages in the centre-right. These languages contain a mixture of gender of speaker and relative gender distinctions, exemplified by cluster C and O. While the UMAP projection appears to show less structure here, than in the previous analyses, the silhouette scores suggests that the clusters are statistically separate in most cases. The two exceptions being cluster C and cluster O. Cluster C shows large overlap with cluster M, which are identical asides from one structural feature (relative gender term for sister's son). Cluster O is between two very different clusters - B and E, suggesting cluster O may not represent a single organisation, and should be analysed with caution.

Table 5.5: Clustering results for G^{-1} kin types. Labs. indicates the identifying number, N is the frequency of occurrence, Div. is the Simpson's index diversity score. Description offers a written description of the cluster. Notation is a description using kinship notation. Silh. is the silhouette score for that cluster.

Lab.	**N**	**Div.**	**Description**	**Coded Description**	**Silh.**
A	102	0.80	Gendered Children terms, term for sibling's son, term for sibling's daughter	S D (BS ZS)(BD ZD)	0.99
B	72	0.16	Gendered children terms, single nibling term	S D (BS ZS BD ZD)	1.00
C	43	0.81	Special term for ZS, term for all other male children, and term for female children	(S BS)(D ZD BD) mZS fZS	0.16
D	40	0.59	Unique terms for all relationship	S D BS BD ZS ZD	0.86
E	38	0.79	Single term for child, single term for nibling	(S D)(BS ZS BD ZD)	1.00
F	31	0.80	Gendered children terms, term for brother's children, term for sister's children	S D (BS BD)(ZS ZD)	0.70
G	21	0.67	One term for all niblings and children	(S BS BD ZS ZD)	1.00
H	19	0.72	Daughter separate from male offspring and female offspring terms	(S BS ZS)(ZD BD) D	0.63
I	19	0.66	Single term for children & brother's children, special terms for sister's children	(S D BS BD) (ZS ZD)	0.97
J	18	0.31	Single term for all relatives - but special relationship with males and their sister's children	(S BS BD fZS fZD) (mZS mZD)	0.95
K	16	0.78	Group ego & ego's brothers' children, separate terms for ego's sister's children	(S BS)(D BD)(ZD ZS)	0.84
L	16	0.53	Terms for opposite-gender sibling's children, and gender of speaker distinctions for same-gender sib children	X m// f//	0.69
M	14	0.78	Term for male child and term for female child	(S BS ZS)(D ZD BD)	0.73
N	13	0.27	Single term for child, single term for nibling, term for sibling's son, term for sibling's daughter	(S D)(BS ZS)(BD ZD)	1.00
O	11	0.74	Gender of speaker distinctions for opposite-gender sibling's children, single parallel terms.	// mX fX	0.07
P	10	0.69	One term for male lineage, one term for female lineage	(S BS BD)(D ZS ZD)	0.69
-	117	-	Outlier	-	-

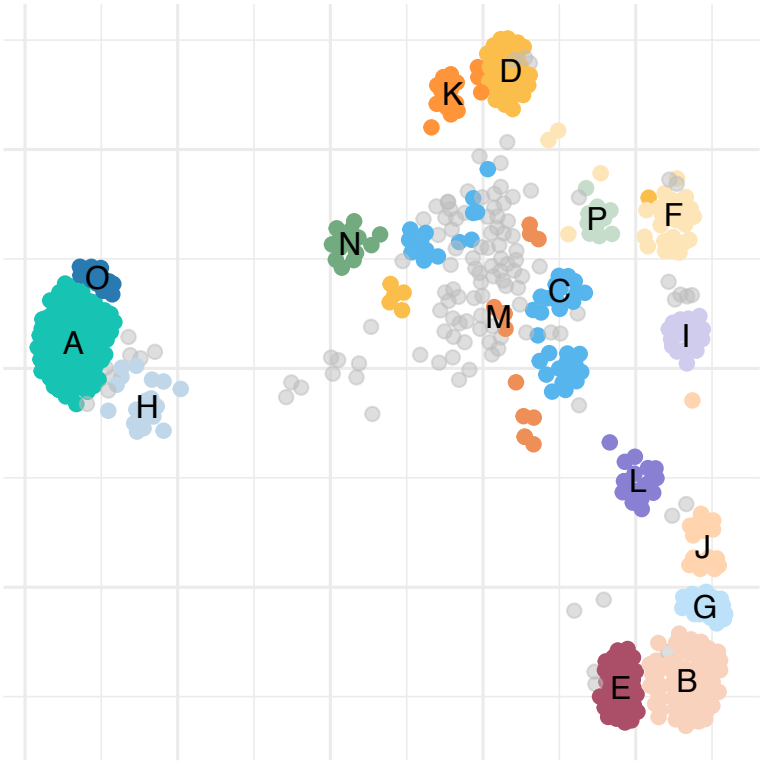


Figure 5.8: UMAP projection of G^{-1}. Despite the large number of unclassified languages, all clusters are identifiably, with the exception of cluster C and O. Clusters B and E form a broader group of organisations separating own children from siblings children. Cluster A also does this, but is very distant in kinspace. This may be because cluster A primarily distinguishes by gender, then distinguishes children from siblings children, creating more differences in the structural vectors and placing them further apart in the space.

5.6.6 Typology summary

The introduction to this chapter provided two hypotheses :

1. Kinspace will reveal clusters of kinship terminology, which can inform typology.
2. Kinspace clusters will not be equally variable

The preceding analysis has quantitatively identified cultural elbows in kinship terminology diversity, which answers confirms hypothesis 1: there are statistically identifiable types of kinship terminology in each subset analysed. However, the identifiability of clusters, and therefore types, varies by subset. In siblings and grandparents there are strict divisions between types, where as in niblings there was considerably more variation in organisation and it was difficult to make clear distinctions. The variation in the distinctions between clusters offers support for hypothesis 2: types are not equally variable. Support for hypothesis 2 is also garnered from the within-type diversity of existing typologies, as seen in G^0, and to a lesser degree in siblings. Within-type variability supports ideas raised by Nerlove and Romney (1967), that rules defining kinship organisation are conditionally invoked (discussed previously in section 4.2.4).

Sibling and grandparent subsets display emergent clusters and are also the two smallest theoretical spaces (table 5.6). The existing sibling typology was well recovered; however, we emphasise the importance of separating reversible types into their own category with the aim of creating a typology that is predictive of social organisation (Nerlove & Romney, 1967). G^{+2} has the smallest theoretical subspace of kinship organisation, and we observe 13 of the 15 possible types. The rule of collaterality predicts that the two unobserved types are not possible in human society. G^{+1} shows the next most identifiable clusters, followed by G^0 and G^{-1}, which show some significant groups, but also areas of high variation.

Notably, in the sibling, G^{+1}, and G^{+2} subsets, the most frequent types populate the edges of the space. The placement types around the edge of kinspace indicate a maximum disparity within observed diversity. In these subsets, the popularity of disparate types may indicate a disparity-first model of kinship terminology evolution, within a cognitive framework (Erwin, 2007). This is an area for future research.

The transparent and algorithmic approach implemented in this chapter has supported some existing typological divisions, but in general, has highlighted that diversity in kinship terminology is much higher that the standing typologies show. Within G^0 and G^{+1}, we find evidence for the six-piece typology used throughout anthropology but find significant variation within these broad groupings (Murdock, 1949). Previous research has suggested localised variation (in respect to kinspace) can align with significantly different social organisations (ie. Dravidian- and Iroquois-types), and work here supports the conclusion that these finer distinctions are an important avenue for future research (Trautmann & Barnes, 1998). G^{-1} is the least separable, giving less confidence in the identification of types and containing a large proportion of

Table 5.6: Summary of theoretical space and observed unique organisation by kin type subset.

Subset	Languages	Unique types	U. Types / Languages	Theoretical Categories
Siblings	849	85	0.100	4,140
G0	503	259	0.515	1.57 x 1,035
G+1	719	91	0.127	5.17 x 1,013
G+2	866	13	0.015	15
G-1	600	96	0.160	5.17 x 1,013

uncategorised languages. Table 5.6 shows the summary of diversity across each subset of kin types.

To make this typology of practical use, computationally derived decision trees are available in appendix C (figure S5.1 - S5.5), to aid with future categorisation of languages. Decision trees are derived directly from the categorisation of languages from HDBSCAN, but could be refined in future to allow for levels of specificity in categorisation, and account for categories that were not deemed to be statistically identifiable *post-hoc*.

5.7 Typological cohesion

Within the existing six-piece typology, there is an assumption of terminological cohesion (Godelier, 2012). That is, how parent's and their siblings are organised is reflected in how their children are categorised. For example: In English, all aunts give birth to cousins, and aunt's giving birth to brother's does not make sense. This inter-generational coherence makes logical sense (particularly as it is reflected in English kinship terminology), but recent research has questioned the strength of this assumption (Passmore et al., In preparation). The recent study showed that, when using the six-piece typology to categorise a language's G^0 and G^{+1} organisation separately, there was only a moderate correlation (i.e. does an *Eskimo-style* organisation in G^0 correlate with a *Eskimo-style* organisation in G^{+1}).More detailed investigation of this correlation revealed that this was likely due to the effect being driven by a strong inter-generational relationship in *Eskimo-type* terminology, and that the relationship was weaker elsewhere (Passmore et al., In preparation).

Research on the Carib-speaking Kuikuru of Brazil explored a similar mismatch of *Hawaiian-style* cousins, and *Iroquois-style* G^{+1}, highlighting the influence of a recent change in population size (Dole, 1969). Here, I explore internal coherence of kinship terminology across more generations and, using our cluster types, with a finer level of granularity between G^0 and G^{+1}, G^{+1} and G^{+2}, and between siblings and niblings.

To test the pattern of co-selection across these pairs, and to remain consistent with previous research, I use Cramer's V tests (Passmore et al., In preparation). Cramer's V varies between 0 and 1, where 1 indicates a perfect association. The statistics are as follows: between G^0 and G^{+1}: 0.359 ; between G^{+1} and G^{+2}: 0.244, and between siblings and niblings: 0.336. Under the standardised interpretations, there is a strong association between G^0 and G^{+1} and siblings

and niblings, and a moderate association between G^{+1} and G^{+2} (Cohen, 1988). Since previous research suggests that *Eskimo-types* produce strong inter-generational effects, which might inflate the strength of the general effect, I explore the strength of particular relationships below using conditional probabilities (Passmore et al., In preparation).

Conditional probability assumes some level of directionality in kinship co-selection by asking the question, for example, what is the probability of having a cross-cousin distinction in G^0, given a bifurcate merging organisation in G^{+1}. Theoretically, conditional probabilities can be calculated in both directions but analysing the relationship in a heritable pattern (i.e. parent's kin terms inform child's kin terms) appears a more logical relationship and aligns with reproductive relationships.

Specifically the probabilities being calculated are: what is the probability we can predict organisation in G^{+1} given we know the organisation in G^{+2}, what is the probability we can predict organisation in G^0 given G^{+1}, and what is the probability we can predict organisation in niblings given sibling organisation. I only discuss conditional probabilities that are of theoretical interest and occur more than ten times.

5.7.1 G^{+2} and G^{+1}

Between G^{+1} and G^{+2} 44 of 72 possible cluster pairings occur, but the only frequent pairings involve G^{+2} cluster A (coded as: [FF MF][FM MM]) and B ([FF MF FM MM]). Cluster A's strongest relationship to G^{+1} is with cluster A (M F (FB MB) (FZ MZ); $\boldsymbol{P(A_{+1}|A_{+2}) = 0.314}$), followed by cluster B (M F MB MZ FB FZ; $\boldsymbol{P(B_{+1}|A_{+2}) = 0.243}$), and finally cluster C ((M MZ)(F FB) FZ MB; $\boldsymbol{P(C_{+1}|A_{+2}) = 0.0980}$). Cluster A is also linked to D, E, F, G, and J, but with very low conditional probability. G^{+2} cluster B strongest relationship is also with G^{+1} cluster A ($\boldsymbol{P(A_{+1}|B_{+2}) = 0.368}$), and secondly with cluster C ((M MZ)(F FB) FZ MB; $\boldsymbol{P(A_{+1}|B_{+2}) = 0.226}$). I draw two conclusions from these patterns 1) there is some evidence of constrained organisation (i.e. bifurcate-merging grandparent organisation link strongly with bifurcate merged G^{+1} organisation), but that these strong connections are type specific, and 2) Descriptive or *Sudanese-type* terminology are flexibly paired with any other terminology.

5.7.2 G^{+1} and G^0

Between G^0 and G^{+1} we observe 99 of 192 possible cluster pairings, but high frequency relationships only occur within G^{+1} cluster C ((M MZ)(F FB) FZ MB) and A (M F (FB MB) (FZ MZ)), which are exemplary Iroquois-type and Eskimo-type G^{+1} organisations respectively. Cluster C has one link exceeding our frequency constraint, with G^0 cluster E (X // (FZS FZD MBS MBD); $\boldsymbol{P(E_0|C_{+1}) = 0.25}$). Both these clusters contains a patterns of crossness, making a logical pair. The sibling and parallel cousin organisation however is unusual - but exploring this cluster shows that this is mostly driven by a set of Sungwadia dialects from Vanuatu, which all have the same kinship organisation. Cluster C shows three links to G^0 cluster A (eG

yG (FBS FZS MBS MZS FBD FZD MBD MZD); $P(A_0|C_{+1}) = 0.265$), C (B Z (FBS FZS MBS MZS)(FBD FZD MBD MZD); $P(C_0|C_{+1}) = 0.159$), and B (eB yB eZ yZ (FBS FZS MBS MZS FBD FZD MBD MZD); $P(B_0|C_{+1}) = 0.124$). All of these were identified as Eskimo-type organisations, but have varying sibling organisations. From these results we see stronger evidence of co-selection, but again this appears to be driven by a few very strong links, with most pairings very infrequent.

5.7.3 Siblings and niblings

Between siblings and niblings, 87 of 224 possible cluster pairings are observed, but many of which are infrequent. Sibling organisations that show frequent links are cluster F ((eB yB eZ yZ)), A (eB eZ yB yZ), C ((eB yB) (eZ yZ)), and B ((eB eZ)(yB yZ)). Sibling cluster F is linked with nibling cluster B (S D (BS ZS BD ZD); $P(B_{-1}|F_0) = 0.40$). Sibling cluster A is linked with niblings cluster A (S D (BS ZS)(BD ZD); $P(A_{-1}|A_0) = 0.351$), and cluster C ((S BS)(D ZD BD) mZS fZS; $P(C_{-1}|2_0) = 0.196$). Sibling cluster C is linked with nibling cluster A ($P(A_{-1}|C_0) = 0.462$), and D (S D BS BD ZS ZD; $P(D_{-1}|C_0) = 0.212$). Finally, sibling cluster B is linked with nibling cluster B ($P(B_{-1}|B_0) = 0.638$). Sibling cluster F shows logical links where the absence of gender distinctions in siblings is maintained in siblings children. However, in the presence of relative age distinctions, we do not observe any organisation that maintain this pattern in descending generations (i.e. $eBD \neq yBD$ is never observed).

The result here align with existing work - overall there is a strong or moderate statistical relationship between generations, the statistics are driven by a few specific links rather than a general principle of integenerational dependence. As suggested by Nerlove and Romney (1967) (see section 4.2.4), some primary rules impose stronger patterns of co-selection that others. *Eskimo-style* organisations seem to impose strong co-selection patterns on descending generations (as is seen in English), but *Sudanese-type*, or descriptive, terminologies are flexibly paired with most other organisations. It is important to acknowledge that the statistics in this section do not control for patterns of historical and horizontal relationships, which may overemphasise the links between organisations. By discussing each of the observed connections I have tried to mitigate the impact of language interdependence, and identify when probabilities are driven by single language family clusters, but caution with these results is still necessary.

5.8 Understanding kinspace

Approximating kinspace provided the opportunity to quantitatively analyse observed kinship diversity, however, in order to build a predictive and evolutionary account of how languages are distributed and move throughout the space there needs to be a theoretical model of change. Previous work has suggested Optimality theory as a good model for describing variation and change in kinship terminology (Jones, 2010, and as discussed in 1.2.2). Using both the identified

clusters and the idea of a minimum rule change, I build a network between the observed clustered following rules of cognitive drift, or minimal change (Viveiros de Castro, 1998). Under a model of cognitive drift, the frequency of any particular type may be influenced by its position in the network. Kinship terminology which are heavily connected are more likely to occur that periphery types if terminology language is not influenced by any external forces. After building this model, I test how well it approximates the relationship between languages in kinspace, and then, how well the network predicts the global diversity of kinship types.

In section 4.2.5, I proposed a theoretical model of change based on Optimality theory (OT). This model uses the rank order of rules to infer the likelihood of change between kinship terminology types. Importantly any OT rule that describes a terminology can change, and each change is weighted by the rank order of that rule (higher ranking rules are less likely to change), ultimately creating a completely connected network between all possible kinship terminology. Computational demands require a scaled down version of this model. Using only the identified typology in section 5.6 and minimum rule change (rather than weighted and all possible changes), I build a network between each identified type. Since the networks are entirely connected, changes are possible between all types, but practically, multiple changes are necessary to get between organisations without a direct link. Using a sibling subset as an example: English has two terms (brother and sister) that cover the eight possible kin types, which can be described by the activation of a single rule *Distinguish Gender*. If a secondary rule is activated, *Distinguish Age*, English categorisation a change to a unique term for elder brother, elder sister, younger brother, and younger sister. This change is described using a single link in the network (figure 5.9, red line). Assuming that rule rank is an indicator of likelihood of change - we predict it is more likely that English is more likely to adopt a relative age rule than it would adopt a *relative gender* rule (i.e. [X //] in the sibling analysis). For English to adopt relative gender distinctions, first the language must lose the *Distinguish gender* rule (the highest ranked rule) and introduce *Distinguish relative gender* in its place, a minimum of two links in the network (blue lines in figure 5.9).

I identify all possible single rule changes between the identified types for each set of kin types analysed. The identification of these rules creates a network of likely change between all types (figure 5.10 shows this network for sibling organisation, all other networks are the Appendix C, figures S5.6 - S5.9). In this figure types are nodes and labelled by their description, edges are rule changes and are labelled as such. Rules can be complete or partial changes - to extend the English sibling example, the addition of *Distinguish relative age* creates four sibling terms and represents a full change, whereas a partial change would only see relative age distinctions in one gender (e.g. type 3 or 5) - partial changes are indicated by an asterisk (*). No assumptions are made on the directionality of change.

As discussed in section 4.2.5, existing cognitive research has shown that some features of kinship terminology are easier to learn than others (e.g. conjunctive vs disjunctive categories)

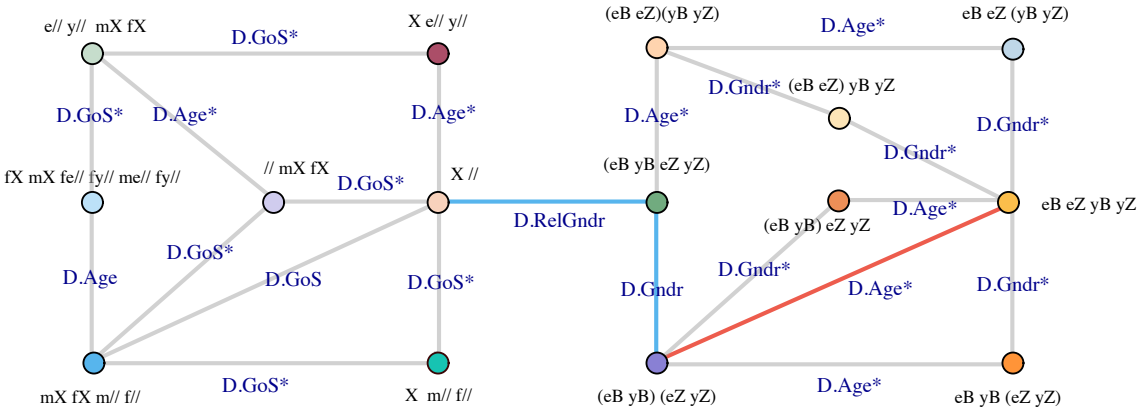


Figure 5.9: Network of minimal change for siblings. Here each node is a type described in table 5.1. Each edge is assigned a rule which is given on each line in purple. In this network there are four rules total, which are either completely or partially implemented: Distinguish Gender (D.Gndr), Distinguish Gender of Speaker (D.GoS), Distinguish Age (D.Age), and Distinguish relative Gender (D.RelGndr). Partial rules are indicated by an asterisk (*). The red and blue lines related to the in-text example. If a relative age rule was introduced in English, this is a single change in the network (red line). If English were to change to a relative gender distinction, this would require two changes (blue lines). Networks for all other subsets can be found in Appendix C.

(Bruner, 1986). The learn-ability of different features means that some links are more likely to occur than other links. To account for this I introduce weights to the network based on existing theoretical models of change. Links are weighted based on three components: the rank of the changing rule (primary, secondary, etc), whether the rule is conjunctive or relational, and whether the rule is a full or partial change. The higher ranked the rule, the less likely it is to change, as discussed in section 4.2.3 (Jones, 2010). Extending the English example, English is less even less likely to change to a relative gender distinction in siblings, since this requires the change of a primary rule, where adopting a relative age rule is the adoption of a secondary rule. Here, I impose naïve weights using the rank of rules (ie. a primary rule is given a weight of one, secondary a weight of two etc.).

Conjunctive changes are weighted twice as likely to occur than relational. Finally, based on the idea that smaller change is more likely to occur because it requires less linguistic invention, I infer that partial changes are twice as likely to occur than full changes. That is, partial changes often only require the introduction of one new word, where as full changes usually need minimum two new terms. It is likely these weights interact with each other; therefore, an edge weight is multiple of each weight attribute (i.e. all attributes are multiplied together). I test the legitimacy of this network in two ways:

1. Is the network representative of the distances between languages in kinspace?

2. Does this network predict global diversity of types in the sample?

To determine whether a weighted network approach is representative of each kinspace subset, I test whether network distance correlates with distance in kinship space using Mantel tests (table 5.7). The distance matrix to represent kinspace is calculated in the previous empirical section using Jaccard distance. The network distance matrix is calculated by summing the weights on each edge on the shortest path between any pair of nodes. All kin type subsets are found to have a significant correlation between this network and kinship space.

Table 5.7: Mantel tests for each generation testing the correlation between distance in kinspace and distance in the theoretically derived network. Each network has a significant correlation with kinspace in each case.

Subset	**statistic**	**significance**
G^0	0.41	<0.001
G^{+1}	0.55	<0.001
G^{+2}	0.74	<0.001
Niblings	0.58	<0.001
Siblings	0.62	<0.001

The Mantel tests show that the model of change represents distance in kinship space, however, the second test will be able to determine if the network can explain the diversity in terminology structure. The structure of the network implies that some types more likely to occur by a function of their place in the network if terminologies evolve under constrained drift. The idea of constrained drift, over other commonly touted forms of external selection, has been suggested by other kinship theorists (Kryukov, 1998), but not quantitatively tested as far as I am aware. Kinship terminology literature has posited that different sets of kin are susceptible to different patterns of change. For example, sibling terms being exempt from common external forces of marriage or group membership (Jordan, 2011), predicting that drift is likely to have a larger impact on kin subsets less susceptible to external influence.

To test whether network position constrains kinship terminology occurrence, I build a model where diversity scores are predicted by their network strength. Diversity scores are taken from tables 5.1 to 5.5 in the kinspace sections above, and network strength is the sum of weights on the edges attached to a node in the networks developed in the previous section. The model asks whether types that occur globally (i.e. have high level of diversity) are more connected in the network. If this is the case, it is plausible that their increased frequency / diversity is caused by constrained drift through the network. Conversely, poorly connected nodes should be less frequent and less diverse. I use Bayesian linear models and WAIC model comparison to determine whether a simple bivariate model, or models with varying slopes or intercepts, for the different subsets, are most appropriate (McElreath, 2020). A bivariate model between diversity or frequency and network strength test whether the general principal is true. Varying intercepts suggest that the pattern is the same for each subset of kin types, but the effect size is different, whereas varying slopes suggest the effect varies by subset.

Model comparisons show a preference for a random slopes model, but strong secondary support for the bi-variate model (table 5.8). Examining the varying slopes model, shows a significant relationship between network strength and diversity scores in siblings and G^{+2}, although the effect size is small (figure 5.10). This is in line with previous predictions that sibling organisation is largely independent of external pressure (Jordan, 2011) and suggests grandparental terms are similarly less effected by these constraints. In all other subsets there is no apparent relationship between network strength and diversity.

Table 5.8: Model comparison results for the model diversity ~ network strength. Results show a preference for the random slopes model, suggesting that the network predicts diversity better some subsets more than others.

Model	**Diversity**		
	WAIC	**dWAIC**	**Akaike-weight**
Strength + Rnd. Slopes	-4.968	-	0.472
Strength	-4.505	0.463	0.374
Null	-2.306	2.662	0.125
Strength + Rnd Intercepts	1.585	6.553	0.018
Strength + Rnd Int. Slopes	2.425	7.393	0.012

5.9 Summary

The bottom-up quantitative approach to kinship terminology diversity can identify clear clusters of structural similarity in a global sample. These clusters capture some existing typologies (particularly in siblings, and in G^0), but also capture more variability than most existing typologies depict (Murdock, 1949; Nerlove & Romney, 1967). When cross-referencing the identified clusters with existing typologies, the analysis reveals considerable within-type variability. The within type variation observed is often language-family specific. The identification of within-type variation highlights the importance for understanding localised patterns of kinship terminology, and how that might relate to culturally specific environments. Interestingly, there are few examples of transitional types, with most languages in each subset being categorised.

Using the bottom-up defined clusters, I created a network of change based on theories of cognitively constrained drift. This network explains the global patterns of diversity in siblings and in grandparents, suggesting these subsets are less susceptible to external selection pressures, and in turn suggesting the influence of external pressures in G^{+1}, G^0, and G^{-1}.

I argue throughout this paper that establishing the extent of diversity in kinship terminology is essential to understanding the link between language and social organisation. The desire to understand diversity is part of a general trend in linguistics and in anthropology to establish the breadth of difference cross-cultural before drawing universal conclusion (Evans & Levinson, 2009; Hannerz, 2010). An obvious next step after the identification of new terminology types is to assess the predictive ability of the identified types with external predictors of

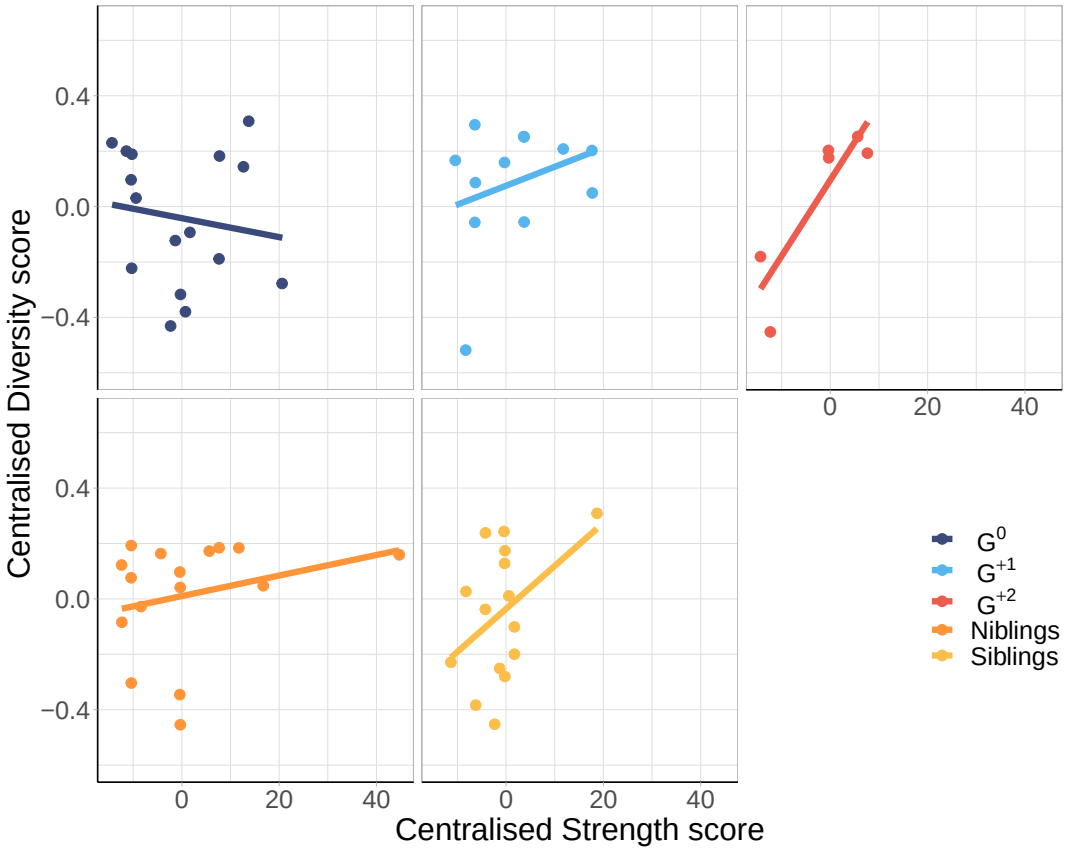


Figure 5.10: Centralised diversity score against centralised strength score, where points are coloured by kin type subset. Lines indicate linear relationship within each sub-type. From top left clockwise: G^0, G^{+1}, G^{+2}, niblings, siblings. Significant relationships are found between G^{+2} and siblings, but no other subset.

organisation, such as marriage or residence patterns. But also exploring the history of types that appear in few languages families and what conditions cause them to be well conserved. Having established this approach in the most common subset of kinship terminology, examining the diversity within affinal categorisation, and between consanguineal and affinal relatives may provide further understanding to the structural diversity in kinship terminology. Affines in particular may reveal interesting patterns between linguistic categorisation and social organisation, with much theory already existing in this area (Godelier, 2012). For example: the co-lexification of affinal and consanguineal relatives is thought to indicate the presence of prescribed cross-cousin marriage (Lounsbury, 1964). Overall, this new approach provides a new avenue to understand the extent of diversity in kinship terminology organisation from a quantitative perspective. Using this new, and quantitatively defined typology, can aim to unravel the complex relationship between kinship terminology to social organisation.

Chapter 6

Kinship and Cooperative Behaviour

6.1 Kin terms and their meaning

Since the discovery of cross-cultural variation in kinship terminology, anthropologists have wondered what these differences represent (Fox, 1979; Hirschfeld, 1986). In the previous chapters, I have approached this curiosity from macro-evolutionary perspective, treating a language as the unit of interest. However, this chapter explores cross-cultural diversity at the level of the kin term, and what the function of kin terms are cross-culturally. For example: In Hindi the term *behan* is used to refer to both a sister and a female cousin, whereas in English these relatives are referred to separately. What makes grouping sister's and female cousin's a coherent category for native Hindi speakers but for an English speaker it seems dissonant?

Anthropological theory proposes that linguistic differences in kinship terminology stem from macro-cultural differences in *social kinship*: the patterns of social organisation that structure society (such as marriage, descent, and residence; Murdock, 1949). Kin terms enact social kinship by prescribing different expectations of behaviour (e.g. care, avoidance, sexual mores) to relatives in each category (Parkin, 2012). Since kinship terminology is linguistically standardised, it coordinates individuals to behave according to the appropriate social norms to particular kin members (Gerkey & Cronk, 2010). The coordination and enforcement of social norms through kin terms result in fitness interdependence, the mutual reliance of individuals for improved welfare, which is thought to lead to an evolutionary advantage (Aktipis et al., 2018).

There are two common types of kin terms: those which group a number of kin types under a single term (classificatory kin term, e.g. the kin term *uncle* refers to the kin types *father's brother*, *mother's brother*, or a *parent's sibling's husband* in English), and kin terms that describe a single kin type (descriptive kin term e.g. *son* only refers to ego's male children).

Classificatory kin terms group relatives from a number of genealogical positions into a single social category, and therefore, also prescribe the same expectation of behaviour (Morgan, 1851). For example: the Maya-Mopan use kin terms to coordinate which relatives are expected to provide child care (*tataa'*: father's elder brother and grandfather) and which do not (*suku'n*: an elder brother and father's younger brother) (Danziger, 1993). Amongst the Maya Mopan, the social categories of kin set a single expectation of behaviour across relatives of varying genealogical distances.

The coordinating function of kinship terminology reinforces local norms and understandings of social kinship (Gerkey & Cronk, 2010). Evolutionary theories of kin selection, on the other hand, predict that altruistic behaviours should be directed towards biologically close kin (Hamilton, 1964). *Biological kinship* proposes that altruistic behaviour is driven by the position of genealogical connections produced through reproduction. The theoretical reasoning underlying biological kinship is Kin-selection theory (Hamilton, 1964). Kin-selection theory predicts that altruistic behaviours are, on aggregate, driven by improving indirect fitness benefits through the preferential treatment of close kin over distantly or unrelated individuals (Hamilton, 1964). The distance of kin is often mediated by other factors, such as age, relative age, and gender, but this study standardises these variables. Kin-selection is operationalised through Hamilton's rule, which predicts that cooperative behaviour will occur when the cost to the co-operator (c) is outweighed by the benefit to the recipient (b), multiplied by their relatedness (r, formulated as: $br > c$; Hamilton, 1964). However, a cooperative preference for genealogical kin is not necessarily driven through indirect fitness benefits; it may be that close genealogical kin possess other characteristics that make them preferable partners, such as close relatives being more likely to reciprocate (Nolin, 2010). Despite uncertainty in the mechanism for a genealogical preference in cooperative behaviour, there is considerable evidence that ties formed through biological kinship moderate cooperation. For example: genealogical distance is predictive of cooperation to some degree in food sharing (Gurven, 2004), fighting (Alvard, 2009), and child rearing (K. L. Kramer, 2010).

Since both social and biological relationships between kin have been shown to be predictive of cooperative behaviour, this chapter is asking: when is behaviour best modelled by biological kinship, and when it is best modelled by social kinship? A notable within-group example is seen in the Lamalera in Indonesia. Amongst the Lamalera food sharing is structured by biological relatedness (Nolin, 2010), but hunting parties are organised by the socially-defined patrilineal descent groups (Alvard, 2003; Nolin, 2010). Social norms are more likely to be followed in situations that are observed by others in the community or family, where ignoring the rules will incur a high social cost (Nolan, 2017), but are often ignored in scenarios where there is an immediate physical threat (or fitness cost). For example, an analysis of eighteen maritime disasters showed that men were more likely to survive than women, and crew more likely to survive than passengers, despite norms suggesting the contrary (Elinder & Erixson, 2012).

Interestingly, social norms can be manipulated when there is the opportunity for direct fitness gain. Yanamamö men have been recorded manipulating social definitions of relatedness in order to maximise potential spouses, despite accurately categorising kin otherwise (Chagnon, 2017).

On the surface, the prescription of homogeneous behaviour towards kin at different genealogical distances appears to create a dichotomy between social and biological theories of kinship. A social model would predict classificatory relatives to be treated equally, but a biological model would predict a preference for the genealogically closer relative - assuming equal costs and benefits. But as discussed through the Lamalera example, the coordination of social kinship organisation and biological ties between relatives are often invoked in specific domains. If we can assume socially defined kinship categories prescribe obligation within a society, it is reasonable to expect behaviour to map onto social kinship categories in situations where social norms are enforced. Whereas, situations where fitness is directly and immediately affected, we might expect biological relationships to be a better predictor of behaviour.

There is likely a considerable amount of cross-cultural variation in how strictly kin terms prescribe behaviour (Kronenfeld, 1974). Surveys carried out in Korea and America show systematic but different preferences for particular cousins, despite both languages categorising the eight possible relatives under a single term; *sa-chon* and *cousin* respectively (Jeon & Buss, 2007; Jeon, Yoon, & Choe, 2008). Similarly, Fanti kin terms show little relationship to prescriptions of behaviour (Kronenfeld, 1974). Despite the counter-factual, there is also considerable evidence in the affirmative, with much anthropological and ethnographic literature linking social norms of behaviour to kin terms (Danziger, 1993; Mitchell, 2015; Trautmann & Whitely, 2012). Experimentally, Yasawan Fijians showed preference for socially defined kin in paired coordination based economic games, as well as a general preference for biological kin, highlighting how cultural and biological forces can work in tandem (McNamara & Henrich, 2017). In general, evidence suggests that the importance of kinship norms, and the extent to which kinship terminology prescribes behaviour, is culturally variable.

Psychological studies on kinship norms and preferences often use languages where social and biological ties make identical predictions (e.g. English and Korean; Jeon & Buss, 2007; Jeon et al., 2008). This makes it impossible to observe the difference of social and biological predictions. Anthropologists have studied more diverse groups, but by studying the behaviour of individuals, the noise of individual preferences and circumstances may bury the norms and expectations within society. Here, I explore this problem in a pre-registered study by comparing expected behaviour between languages where social and biological predictions are the same (English), and one where the predictions are different (Hindi; pre-registration: https://osf.io/su39z). By testing expected patterns of behaviour, rather than individual behaviour, it is possible to explore whether there is a community-wide consensus on the expectations of kin-categories.

6.2 Hypotheses

With significant variation in kinship organisation, parsing the interaction of social and biological kinship can help explain cross-cultural variation in kin-oriented behaviour, but also unveil how the cultural environment interacts with biological predispositions. I reason that the coordinating effects of social kinship and the evolutionary predictions of biological kinship conditionally interact depending on whether the situation calls for social coordination of fitness preservation, which I name *social cost* and *genetic cost*. Social cost is when the cost of not behaving appropriately impacts social standing; for example, not attending a relative's birthday. In the case of classificatory kin terms, social cost will apply to a kin category, rather than genealogical distance. Genetic cost is when there is imminent impact on genetic fitness; for example, having to save a relative from life-threatening situations, but also caring for a relative's offspring (Jankowiak & Diderich, 2000). When genetic cost is acting, less attention is paid to social norms and in particular how violating social norms might affect standing, and more attention is paid to the fitness impact of the impending situation. In this case, more attention is paid to the biological kinship relationships.

I pre-registered two hypotheses based on the interaction of these phenomena:

1. In high social-cost situations, classificatory relationships will be prioritised over genealogical and there will be a difference in behaviour between Hindi- and English-speaking participants

2. In high genetic-cost situations, genealogical relationship will be prioritised over classificatory and there will be no difference in behaviour between Hindi- and English-speaking participants.

These are operationalised in five scenarios (available in the draft survey attached to the OSF pre-registration):

Scenario	**Social cost**	**Genetic cost**	**Previous research**
1: *Birthday parties*	High	Low	(Jankowiak & Diderich, 2000)
2: *Babysitting*	Low	Medium	(Jankowiak & Diderich, 2000)
3: *Moving to a new house*	Low	Low	-
4: *Distribution of inheritance*	High	High	(Judge & Hrdy, 1992)
5: *Providing CPR*	Low	High	(Elinder & Erixson, 2012)

6.2.1 Justification of scenarios

Each scenario aims to place participants in a scenario that should elicit either social- or genetic costs and therefore influence participants behaviour. Attendance at *birthday parties* is a visible social event, therefore social cost is high, but there is little effect on fitness. *Babysitting* on the

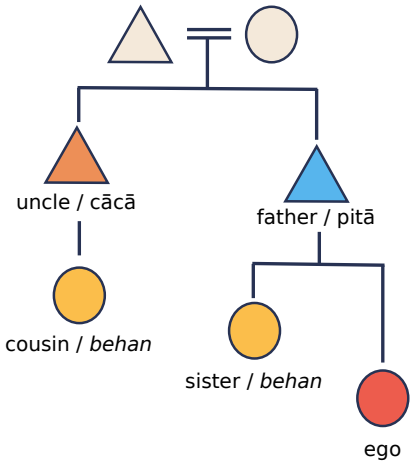
other hand is usually a domestic activity and not particularly visible to others. Babysitting is likely to have a very small impact on fitness, particularly in the western context where this is usually for short periods of time. However, an existing study looking at polygamous Mormon families in the USA found individuals significantly preferring to care for the children of their siblings over their half-siblings, which has a larger inclusive fitness benefit than helping half-siblings (Jankowiak & Diderich, 2000). *Moving to a new house* is both a relatively private activity and has little effect on fitness. *Inheritance of wealth* has both strong social and fitness implications. Studies on the distribution of wealth from testate decedents in California find most wealth passes onto a spouse, and is considerably above the amount that is passed onto a child (Judge & Hrdy, 1992). Since the study is of the deceased, children are often older (average age being 33), so leaving inheritance to spouses is unlikely to improve child outcomes and is likely the result of social norms. Directly investing in children of this age may either increase the likelihood that grandchildren are born (by providing the financial security to do so) or support existing grandchildren. It is reasonable to expect that providing a spouse with resources will indirectly benefit offspring, but if improving fitness was a direct goal of inheritance, then this pattern of investment is inefficient. The *CPR* scenario presents a situation with a direct fitness impact, creating a decision between helping relatives of different genealogical distance. Existing research suggests that when there is considerable danger, self-preservation is the highest priority and social norms are often ignored (Elinder & Erixson, 2012). The CPR scenario will test whether preservation efforts extend to indirect fitness benefits.

6.3 Methods

To test the two hypotheses, participants read a description of a fictional family. They were asked to make decisions for a particular family member in five scenarios reflecting the hypotheses above. The survey was written in English and translated into Hindi, then independently back translated to ensure the meaning was translated accurately. The only difference besides language of presentation between surveys were culturally appropriate names for family members. At the conclusion of each scenario, participants were asked to help the youngest child to split her time or resources between her genealogical older sister, and genealogical older cousin (of similar age). In Hindi, these two relatives are both described as *behan*, but for English speakers they are *sister* and *cousin* respectively (figure 6.1).

6.4 Participants

To test the relative impact of kin categorisation on behaviour I sampled participants from three populations: individuals whose first language is Hindi and respond to the survey in Hindi (Hindi-Hindi), individuals whose first language is American-English and respond to the survey in American-English (English-English), and individuals whose first language is Hindi, but re-



Some time ago a man and a woman got married.

A year after their marriage, they had a son,
and a year and a half after that, another son.
Time has passed and the sons have children of their own.

The first son has one daughter, called Alice,
and the second son has two daughters,
called Emma & Olivia.

Alice was born first, second was Emma, and the youngest is Olivia.

In the next section of the survey you are required to make some decisions for Olivia.
Respond with how you expect someone should behave in each scenario.

Figure 6.1: Kinship diagram: Family organisation described to participants. Triangles indicate men, circles indicate women. Kin terms on the left are in English and right are Hindi. Participants are asked to take the viewpoint of ego and split resources between the cousin and sister (Hindi: *behan*) in a variety of scenarios. Height in the diagram indicates relative age. Ego is the youngest, ego's sister is younger than ego's cousin. Ego's father is younger than ego's uncle. Description: The description that participants read describing the family structure. No kin terms are used that refer to the relationship between ego and the relatives for which she will be asked to split resources. Although it is necessary to describe their parents as brothers.

spond in English (Hindi-English). These populations are sampled from India, the USA, and the USA respectively. The first two populations allowed us to determine whether kin categorisation influences cooperative behaviour (Hindi-Hindi) against an alternative where social and biological predictions are identical (English-English). This was the initial preregistered comparison. Before data collection, the pre-registration was amended to include the third population, Hindi-English. This population is used to determine whether a difference between Hindi-Hindi and English-English is a result of social differences, or a solely linguistic effect. If the effect is purely linguistic, then Hindi-English participants should respond the same as English-English, whereas if it is cultural, then Hindi-English participants should respond more similarly to

Hindi-Hindi participants.

Participants responded to the scenarios via an online survey and were recruited through Prolific (English-English and Hindi-English) and Mechanical Turk (Hindi-Hindi). I attempted to recruit 100 participants for English-English and Hindi-Hindi, and 50 participants for Hindi-English (due to available sample-size restrictions). Metadata from each survey site screened participants based on their first language, however, I also screened participants via a short language proficiency test, an attention check, and a comprehension check. The language proficiency test assured participants have a command of the desired languages and alongside the attention check, screened out bots or rapid responders. The comprehension check assessed whether participants understood the relationship between family members in the description. After the screening process, the participant pool contained 75 English-English participants, 64 Hindi-Hindi participants, and 30 Hindi-English participants.

6.5 Procedure

Participants entered the survey site for their respective language (Hindi or English) and were asked to give consent before the language proficiency test. They then read a short description of the family genealogy, which does not invoke the use of any kin terms used in the study (figure 6.1). Participants can re-read this description at any point throughout the survey.

Participants are told they will help the youngest daughter (referred to by name) make decisions on how to split resources between the daughter's genealogical cousin and genealogical sister (also referred to by name). Participants indicated their preference on a five-point scale. The meaning of the scale is dependent on the scenario, but in all scenarios a response of one indicated that 100% of resources should go to the genealogical cousin, three indicated splitting resources equally, and five indicated giving 100% of resources to the genealogical sister. In scenarios one, two, and three, the resource was time, in scenario four it was money, and scenario five it was relative time. Pilot studies revealed that many participants responded with the middle value (three) for all questions. To assess whether participants had any preference, when a response of three was given, participants were asked a follow up question, asking them to choose between a slight preference for a genealogical sister or a slight preference for a genealogical cousin (i.e. two or four on the previous scale). In the subsequent analysis the forced response variable is treated as a four-point scale. The forced-choice response was not pre-registered.

After completing the scenario response, participants completed a comprehension check, and were asked to provide the kin terms used between all pairs of family members. Should a participant fail the comprehension check (i.e. misunderstand the family dynamics), their data is not included in any analysis. Finally, participants are asked for some basic demographic information (gender and age).

6.6 Results

I built a Bayesian multi-level cumulative ordinal regression to model the results (implemented in brms, Bürkner, 2018). The outcome variable is either the five- (raw response) or four-point (forced-choice) scale in each scenario which is predicted by: population (Hindi-Hindi, English-Hindi, English-English), scenario, gender, and age, as well as a random effect for participant. Using a cumulative ordinal model allows us to assume that the five-point scale represents an underlying continuous variable (in this case kin-member preference) that comes from a normal distribution (Bürkner & Vuorre, 2018). Raw data are shown as a part of figure 6.2, alongside model predictions (model details discussed below).

Both hypotheses are tested using an interaction effect between scenario and population. To test the effect of the interaction, I compared a model with an interaction effect between language and scenario, to a model without, using LOO (Leave-one-out) comparison. The LOO Information Criterion estimates the same expected log predictive density as AIC, but accounts for prior distributions used in the model, as well as not assuming multivariate normal distributions in the posterior (Goodrich, Gabry, Ali, & Brilleman, 2020). I used the LOO output to calculate model weights. Model weights are calculated by minimizing the LOO-mean squared error where all weights sum to one and higher numbers indicate a preferred model (table 6.1). In line with the pre-data collection amendment to pre-registration, models were run under four conditions: without Hindi-English (constituting the original pre-registration) and with the additional group Hindi-English, and modelled the raw data as the outcomes variable (pre-registered response), and the forced choice responses as the outcome variable.

In both the raw response and forced choice models excluding Hindi-English, the LOO model comparison statistics indicated no preference for the interaction model (see table 6.1). When including Hindi-English, there was a strong preference for the no interaction model between scenario and population when modelling the raw response, and no preference when modelling the forced choice response. The non-interaction model was preferred in all cases under an assumption of parsimony - providing support against the pre-registered hypotheses.

I explored the effects of scenario and population on participant response and propose some *post-hoc* explanations. I examined output of the model "With Hindi-English raw-response" model, which compared all three populations in all five scenarios. The output for all models can be found in Appendix D, tables S6.2 - 6.9. The "Hindi-English raw response" showed two effects: a significant difference between Hindi-Hindi and English-English populations, and an independent significant difference in responses to inheritance and CPR scenarios when compared to the moving-house scenario (table 6.2). Since we used cumulative ordinal regression, all models have multiple intercepts, which are the cumulative log-odds of each response value and maintain the ordinal nature of the response variable.

To quantify the significant difference between Hindi-Hindi and English-English, I calculated the odds ratios for a preference of genealogical sisters (allocation >3) and equal treatment of

Table 6.1: Model comparison results between two subsets of the model across four subsets. Weights are calculated by minimising the LOO-mean squared error of each model, and sum to 1. Without Hindi-English and raw response is the original pre-registered dataset, where there is no preference for the predicted interaction model over a non-interaction model. There is no preference for an interaction model when using a forced choice response. There is a strong preference for no interaction when including Hindi-English and using a raw response, although this preference disappears when using the forced choice response.

	Model weights	**No interaction: Language + Scenario**	**Interaction: Language * Scenario**
Without Hindi-English	Raw response	0.50	0.50
	Forced Choice	0.50	0.50
With Hindi-English	Raw response	0.94	0.06
	Forced Choice	0.48	0.52

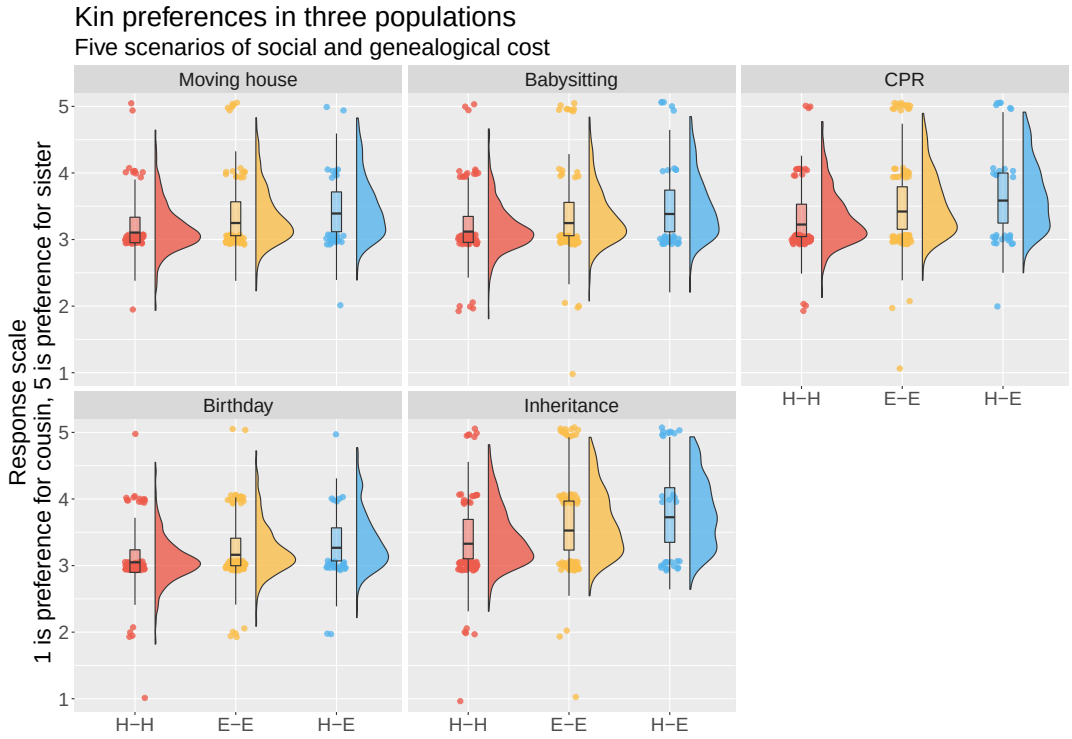


Figure 6.2: Each plot contains the raw data (coloured points) and model prediction (boxplot and density plots). Raw data is ordinal ranging from 1 - 5. Model predictions are from the no-interaction model including Hindi-English populations. Model prediction data is the predicted average score by groups and scenario from 500 posterior samples. H-H refers to the Hindi-Hindi population, E-E to English-English, and H-E to Hindi-English. Plots are ordered so genetic cost is increasing from left to right, and social cost is increasing from top to bottom. Alignment in the grid does not equate to equivalent cost (i.e. the genetic cost for babysitting and inheritance is not considered equivalent).

Table 6.2: Model output for the "with Hindi-English" raw response model. The baseline comparison for the language population variable is English-English, and the baseline for the scenario variable is Moving house. Predictor variables with 95% CI that do not contain zero are in bold. This shows the significantly lower response between Hindi-Hindi and English-English responses, and the significant preference for genealogical sisters in the inheritance and CPR scenarios.

Parameter	**Estimate**	**S.E.**	**Lower 95% CI**	**Upper 95% CI**
Intercept 1 - 2	-5.34	0.78	-6.67	-4.11
Intercept 2 - 3	-3.04	0.66	-4.12	-1.94
Intercept 3 - 4	2.37	0.64	1.34	3.49
Intercept 4 - 5	4.27	0.67	3.20	5.42
Hindi-Hindi	**-0.70**	**0.32**	**-1.23**	**-0.21**
Hindi-English	0.48	0.42	-0.20	1.14
Babysitting	0.03	0.26	-0.39	0.47
Birthday party	-0.40	0.25	-0.81	0.02
Inheritance	**1.05**	**0.25**	**0.66**	**1.46**
CPR	**0.65**	**0.25**	**0.23**	**1.07**
Gender (M)	0.35	0.31	-0.14	0.87
Age (continuous)	0.02	0.01	0.00	0.05

relatives in each group (allocation = 3; very few people preferred genealogical cousins). I then calculated the odds ratio between populations, holding other predictors constant: age at 30 years old (average age), gender as male, and moving house as the baseline scenario. The odds ratios found that English-English participants preferred genealogical kin 1.59 times (95% CI 1.57, 1.61) more than Hindi-Hindi speakers (Appendix D, table S6.1). To quantify the size of these effects on the allocations, I drew samples from the posterior and calculated the average score for a Hindi-Hindi and English-English participants (displayed in figure 6.2). Across all scenarios, English-English participants scored 0.18 higher than Hindi-Hindi participants on the five-point scale.

To quantify the effect size of a genealogical preference of kin by scenario I performed the same odds ratio procedure above, holding English-English as the referent population. This found that across all scenarios there was a preference for the equal treatment of kin, but the strength of this preference varies by scenario. I found that in the moving house; babysitting; and birthday scenarios, participants are between 2.3 and 3 times more likely to treat kin equally than to show a preference to genealogical sisters. In the inheritance scenario the preference for an egalitarian response reduced to a 1.2 times preference and in CPR a 1.5 times preference for equal treatment.

6.7 Discussion

This study finds no support for the pre-registered hypothesis that social and biological predictions of kin organisation interact to coordinate behaviour. However, the model revealed the influence of social and biological effects independently. The model found that Hindi-Hindi speakers generally expected genealogical sisters and genealogical cousins to be treated more equally than participants who took the survey in English, in line with the social categorisation of those relatives under the term *behan*, in the Hindi language. There was an independent effect of scenario, showing that responses with immediate and direct effect on fitness (inheritance and CPR) showed a preference for genealogical sisters over genealogical cousins (table 6.2).

In the pre-registration, I predicted that social and biological kinship relationships would be conditionally invoked, depending on the scenario. Instead, there was a constant preference for genealogically closer kin, which was mediated by different social categorisation of kin. The differences between populations can be ultimately explained as a culturally adaptive response, and cognitive-linguistic offered a proximate explanation. Below I set out the argument for each interpretation.

6.7.1 Cultural effect

Comparing the response between Hindi-Hindi and English-English participants showed a significant, if small, difference. The more egalitarian responses of Hindi-Hindi speakers reflect the categorisation of sister and cousin under the term *behan*, and highlighted the importance of considering a culturally relative understanding of kin when analysing cross-cultural patterns of kin-oriented behaviour. We believe this is the first direct cross-cultural test of this comparison, and supports observational accounts and experimental results (Danziger, 1993).

While we observe a cultural difference in categorisation and behaviour, this study does not reveal why socially relative kin categorisation exists, and what evolutionary advantage it may contain. A combination of demographic research and the theory of fitness interdependence provides some light on this (Aktipis et al., 2018). Demographic research shows improved health outcomes for young Indian women living in extended patrilocal families, over nuclear families (Allendorf, 2013). Young women in extended families were more likely to use antenatal care and utilise professional birthing assistance, have improved diets, and report less physical violence. Living with extended families in India also sees improved health outcomes for the elderly (specifically grandparents Samanta, Chen, & Vanneman, 2015). While these studies do not identify direct fitness outcomes from living in an extended family (i.e. more children) improved access and use of healthcare and extended support networks are likely to be of some reproductive advantage. Improved health benefits in extended families, who we assume use the classificatory kinship terminology found in Hindi and throughout other languages on the Indian subcontinent, provides some indirect evidence of an evolutionary advantage in maintain-

ing broader kinship ties, which are operationalised through classificatory kin terms. Kin terms are then indicative of fitness interdependence, under a cultural evolutionary model (Cronk et al., 2018). Fitness interdependence, the mutual reliance of individuals for improved welfare, through kin terms in India (e.g. *behan*) creates more individuals with whom close kin ties are created and from who there are culturally enforced adaptive norms (Aktipis et al., 2018).

No effect between English-English and Hindi-English participants could be explained through the Hindi-English participants adapting to new cultural environments (i.e. since they live in the USA). If we can assume Hindi-speaking populations living in the USA adopt local living arrangements (i.e. nuclear families), interdependence with cousins will be reduced relative to their Hindi-Hindi counterparts. Similar effects are seen amongst the Congolese hunter-gatherers, the BaYaka. BaYaka who are born and raised in forest regions have superior plant knowledge to those who are born and raised in logging towns (Salali et al., 2020). If adapting to the local environment is also happening in this study, then we would expect Hindi-English participants who moved to the USA to be more similar to Hindi-Hindi participants, and individuals who were raised in America to be more similar to English-English participants. Unfortunately, I did not collect this information.

6.7.2 Linguistic effect

Where the cultural effect offers an ultimate explanation, linguistic theory offers a proximate explanation. Finding no difference between Hindi-English and English-English populations shows the effect of linguistic categorisation on response and aligns itself with the emerging theories of perceptual cue integration and category bias (Regier & Xu, 2017). Perceptual cue integration suggests that the perception of any particular object is the probabilistic influence of two cues: the first cue being existing experience of that object and the second being the linguistic designation of that category. Category bias occurs when an individual is forced to rely on the linguistic designation of an object over experiencing that cue. The result of this survey indirectly speaks to category bias, which could potentially explain the similarity between Hindi-English and English-English populations, as well as the difference between Hindi-Hindi and English-English populations. By asking individuals to rely on their expectations of behaviour (rather than their own familial relationships), participants must rely on linguistic categorisation to guide their response. Under a cognitive bias rule, we would expect similarity in populations who are using the same linguistic categorisation (i.e. English-English and Hindi-English) and differences to those with different categories (i.e. Hindi-Hindi). To parse the culturally adaptive and category bias effects, an additional population of Hindi speakers taking the survey in Hindi and raised in the USA would be needed. Existing research on perceptual cue theories primarily focus on colour terms or abstract concepts (Cibelli, Xu, Austerweil, Griffiths, & Regier, 2016), however, a more direct, and pre-registered test using kinship terms and terminology might be another domain to test this theory in. It is worth highlighting that Indian-English and

American-English are their own varieties of English, and may not exactly map onto each other, however there is currently no evidence to suggest this reflects differences in kinship terminology.

6.7.3 Biological effect

Finding a scenario specific effect highlights the contextual nature of genealogical relatedness on cooperation. The influence of genealogically defined relationship, and the indirect fitness benefit it provides, has historically been the primary hypothesis for the evolution of wide-spread cooperation, however, it has become increasingly clear that there is considerable cross-cultural variation in the level of cooperative behaviour (Henrich et al., 2005), and that cooperative behaviour has domain specific constraints (Nolin, 2011). Here, I found greater preferential treatment of genealogical kin in CPR and inheritance scenarios, when compared to the moving house, babysitting, and birthday party scenarios. I tentatively propose the key difference between these scenarios is that of reciprocity. Where moving house, babysitting, and birthday party attendance are all situations where one might expect reciprocity of some kind in the future, reciprocity in inheritance is usually unexpected (although could be expected when coupled with a belief in the afterlife), and reciprocity in CPR is a rare occurrence and unwanted reciprocity.

6.8 Summary

The results of this study found no evidence of an interaction between cultural kinship and biological kinship, as was predicted in the pre-registration. However, it did uncover independent evidence of cultural and biological kinship. I reason that the cultural effect reflect the fitness interdependence between relatives and are culturally adaptive (Cronk et al., 2018). A proximate explanation of the cultural effect may be category bias, where individuals rely on linguistic categories of kin in the absence of other information (Regier & Xu, 2017). Biological effects are explained through indirect fitness benefits, and how reciprocity might be a key mechanism in explaining this relationship. However, more specific analysis would be needed to verify these claims. The finding of a context specific effect of kin-selection highlights the temporal complexity of cooperative behaviour, and its relationship to Hamilton's rule. The conclusions drawn in this experiment however fall outside the remit of the pre-registered hypothesis.

Chapter 2 App

Appendix A: Supplementary Material for Chapter 2

Supplementary Material

Sam Passmore and Fiona Jordan

25 June 2020

Table of Contents

Data

Kinship and social structure

All data was extracted from the D-PLACE Ethnographic atlas GitHub repository. Counts of the number of societies used for the signal and ancestral state analyses for each language family are in table S1. Question and variable codes are displayed below in table S2, frequency of terminology types are show in figure 2. Due to the nature of the analysis, all variables are binary coded. The numbers in the value columns indicate the criteria for a society to have the terminology or social structure coded as present. For details on what each code indicates, refer to the Ethnographic Atlas codebook or the D-PLACE GitHub repository.

Table S1: Count of societies in signal test and ancestral state analyses, by language family

	Count
Austronesian	85
Bantu	69
Uto-Aztecan	22

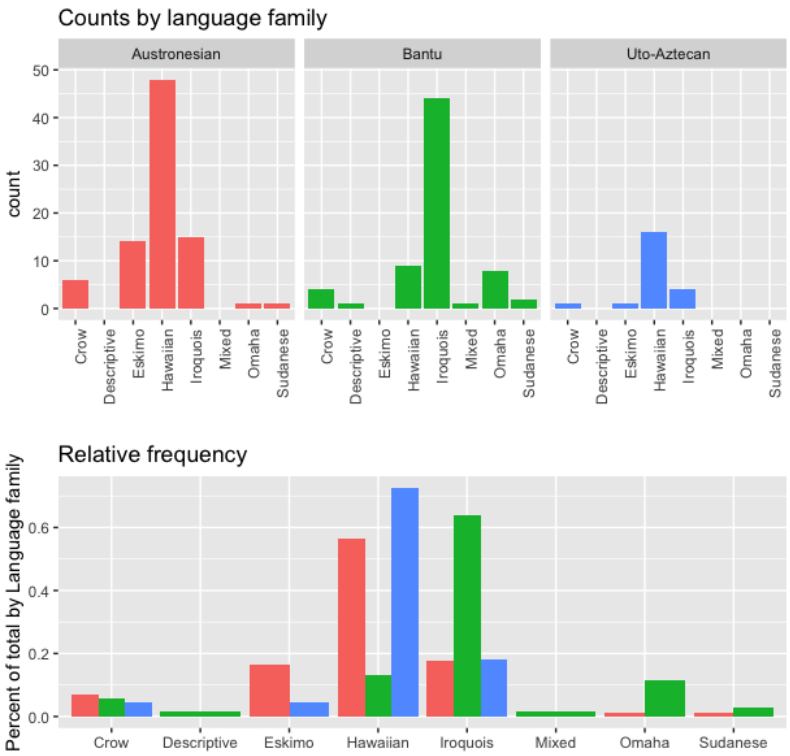


Figure S1: The count and relative frequency of terminologies in each language family.

Table S2: Data coding taken from D-PLACE and Co-evolutionary analyses data counts

terminology	question	value	social structure	question	value	AN	BT	UA
Crow	27	1	matrilineal	43	3	85	69	
Crow	27	1	high.polygyny	9	3,4,5,6	80		
Crow	27	1	polygyny	9	2,3,4,5,6	80		
Crow	27	1	matri.anvunclocalresidence	10	1,5,9	84	69	
Crow	27	1	uni.localresidence	10	1,5,8,9,10	84	69	
Eskimo	27	3	bi.linealdescent	43	2,5,7	85		
Eskimo	27	3	uni.linealdescent	43	1,3,4	85		
Eskimo	27	3	absenceofcousinmarriage.permitted	25	10,11,15	79		
Eskimo	27	3	absenceofcousinmarriage.preference	23	7,8,11,12	79		
Eskimo	27	3	monogamy	9	1	80		
Eskimo	27	3	neo.localresidence	10	6	84		
Eskimo	27	3	nuclear.families	8	1,2	83		
Hawaiian	27	4	bi.linealdescent	43	2,5,7	85	69	23
Hawaiian	27	4	bi.localextendedfamily	8	6,7,8	83	69	22
Hawaiian	27	4	absenceofcousinmarriage.permitted	25	10,11,15	79	66	19
Hawaiian	27	4	absenceofcousinmarriage.preference	23	7,8,11,12	79	66	19
Hawaiian	27	4	bi.localresidence	10	2,11,12	84	69	22
Iroquois	27	5	exogamy.unilineal.descent	15	4	78	62	19
Iroquois	27	5	uni.linealdescent	43	1,3,4	85	69	23
Iroquois	27	5	cross.cousinmarriage.permitted	25	1,6,9	79	66	19
Iroquois	27	5	cross.cousinmarriage.preferred	23	1,2,3,5,6,8,12,13,14	79	66	19
Iroquois	27	5	high.polygyny	9	3,4,5,6	80		22
Iroquois	27	5	polygyny	9	2,3,4,5,6	80		
Iroquois	27	5	matri.anvunclocalresidence	10	1,5,9	84	69	22
Iroquois	27	5	uni.localresidence	10	1,5,8,9,10	84	69	22
Omaha	27	6	patrilineal	43	1		69	
Omaha	27	6	matri.anvunclocalresidence	10	1,5,9		69	
Omaha	27	6	uni.localresidence	10	1,5,8,9,10		69	

Co-evolutionary hypotheses and references

Table S3: hypotheses from earliest found source with quotes, references and page numbers

terminology	hypotheses	quote	justification	reference
Crow	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Crow	Matri-avunculocal residence	"Crow systems should occur more frequency in societies which are avunculocal …"	Avunculocal residence means married couples move to live with the husband's mother's brother and are spatially closer to maternal kin, meaning there is more pressure to specifically identify maternal kin, and paternal kin can be grouped together. With specific reference to Crow societies, it is likely that this also aligns with matrilateral cross-cousin marriage.	Eyde, D. B., & Postal, P. M. (1961). Avunculocal and Incest: The Development of Unilateral Cross-Cousin Marriage and Crow-Omaha Kinship Systems. American Anthropologist, 63(4), 747–771.
Crow	Matrilineal	"The tables show a strong correlation between Omaha terms and patrilineal unilineal descent groups and between Crow terms and matrilineal unilineal descent groups"	A matrilineal descent system imposes a higher social status (social differential) on maternal kin, and therefore the need to distinguish maternal kin over paternal. This allows the grouping of paternal kin.	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Crow	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Crow	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate terms tend to be applied to relatives of the same generation who are linked to ego through connecting relatives of a different sex."	A unilocal residence rule brings into proximity a group of relatives linked under one line of decent. This rule acts as a social differential to support bifurcation of cousin terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Eskimo	Absence of CM permitted	"Prohibition on cousins vary [in Eskimo-types], but as one might expect, are inevitably bilateral"	If all cousins are unmarriageable, there is no social differential and therefore no need to distinguish them	Fox, R. (1967). Kinship and Marriage: An Anthropological Perspective. Cambridge University Press.
Eskimo	Absence of CM preference	"Prohibition on cousins vary [in Eskimo-types], but as one might expect, are inevitably bilateral"	If all cousins are unmarriageable, there is no social differential and therefore no need to distinguish them	Fox, R. (1967). Kinship and Marriage: An Anthropological Perspective. Cambridge University Press.
Eskimo	Bi-lineal descent	"…there is a distinct association of Eskimo terms with bilateral [descent] systems"	When terms differentiate between full siblings and cousins when they are socially differentiated (in this case it is proposed to reflect direct patterns of inheritance).	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Eskimo	Monogamy	"The following variables are dependent upon diverging devolution (transmission of property to both males and	When there is a social focus on the monogamous nuclear family, there is a need to distinguish children	Goody, J., Irving, B., & Tahany, N. (1970). Causal Inferences Concerning Inheritance and

		females): greater control of women's' marriage (prohibition of premarital sex, endogamy, father's brother's daughter marriage, monogamy, alternative residence) and by extension Eskimo kinship terminology which isolates the sibling group form "cousins""	and siblings from other closely related nuclear families.	Property. Human Relations, 24, 295–314.
Eskimo	Neo-local residence	"Neolocal residence tends to be associated with kinship terminology of the lineal type."	Neo-local residence results in the spatial separation of lineal relatives from all collateral relative, and emphasizes the residential group	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Eskimo	Nuclear families	"In the absence of clans and polygamous and extended families, the isolated nuclear family tends to be associated with kinship terminology of the lineal type."	The isolation of the nuclear family operates as a social differential and favours separate terms for the lineal and collateral kin.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Hawaiian	Absence of CM permitted	"Hawaiian [kin] terms … are associated with the prohibition on [cross] cousin marriage"	If all cousins are unmarriageable, there is no social differential and therefore no need to distinguish them	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Hawaiian	Absence of CM preference	"Hawaiian [kin] terms … are associated with the prohibition on [cross] cousin marriage"	If all cousins are unmarriageable, there is no social differential and therefore no need to distinguish them	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Hawaiian	Bi-lineal descent	"Bilateral kindreds tend to be associated with kinship terminology of the generation type"	If there is no social differential between maternal or paternal relatives, nor is there a pressure to distinguish nuclear family from other kin, then there is no pressure to linguistically distinguish siblings and cousins, or parents, and parent's siblings.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Hawaiian	Bi-local extended family	"The several types of extended family … depend upon the prevailing rule of residence and exert the influences upon kinship nomenclature already set forth in Theorems 6 and 11"	Extended families increase social participation and interdependence within society and therefore emphasise the effect of bi-lineal descent.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Hawaiian	Bi-local residence	"Bi-local residence tends to be associated with kinship terminology of the generation type"	Bi-lineal decent brings together some lineal kin, and some collateral kin, some through men and some though women. All these groups combined are then all overridden, and individuals are treated equally.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Iroquois	Cross CM permitted	"Iroquois [kin] terms … are associated with preferred cross-cousin marriage"	If cousin marriage is allowed (or preferred) in some but not all cousins, there is a pressure to linguistically distinguish those who are marriageable from those who are not.	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Iroquois	Cross CM preferred	"Iroquois [kin] terms … are associated with preferred cross-cousin marriage"	If cousin marriage is allowed (or preferred) in some but not all cousins, there is a pressure to linguistically distinguish those who are marriageable from those who are not.	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Iroquois	Exogamy & unilineal descent	"In the presence of exogamous matrilineal or patrilineal lineages, sibs, phratries, or moieties, terms for lineal relatives tend to be extended, within the same sex and generation, to collateral kinsmen who would be affiliated with them	Kin that are members of the same exogamous unilinear group are socially equalized with collateral kin and are therefore terms are merged.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.

		under either unilinear rules of descent."		
Iroquois	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Iroquois	Matri-avunculocal residence	"Matrilocal and avunculocal residence tend to be associated with kinship terminology of the bifurcate merging type"	Avunculocal residences aligns relatives so that the distinction of collaterally is minimized and there is a tendency to extend kinship terms from lineal to collateral co-residing relatives.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Iroquois	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship terms. This results in different terms for parent's opposite sex sibling terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Iroquois	Uni-lineal descent	"The classic but erroneous anthropological view concerning the nature of the 'Iroquois type' of kinship … is that this kind of system classifies kin by membership in unilineal descent groups"	?	Lounsbury, F. G. (1964). The structural analysis of kinship semantics. Mouton.
Iroquois	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate terms tend to be applied to relatives of the same generation who are linked to ego through connecting relatives of a different sex."	A uni-local residence rule brings into proximity a group of relatives linked under one line of decent. This rule acts as a social differential to support bifurcation of cousin terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Omaha	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal kinship terms. This results in different terms for parent's opposite sex sibling terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Omaha	Matri-avunculocal residence	"Matrilocal and avunculocal residence tend to be associated with kinship terminology of the bifurcate merging type"	Avunculocal residences aligns relatives so that the distinction of collaterally is minimized and there is a tendency to extend kinship terms from lineal to collateral co-residing relatives.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.
Omaha	Patrilineal	"The tables show a strong correlation between Omaha terms and patrilineal unilineal descent groups and between Crow terms and matrilineal unilineal descent groups"	Patrilineal descent acts as a social differential between maternal and paternal kin, allowing more terminological distinction between patrilineal relatives, and grouping of matrilineal relatives.	Goody, J. (1970). Cousin Terms. Southwestern Journal of Anthropology, 26(2), 125–142.
Omaha	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the bifurcate collateral type"	Polygyny spatially separates lineal relatives, meaning women are surrounded by co-wives and not sisters, and children by half-siblings and not parallel cousins, which prevents merging of lineal	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.

			kinship terms. This results in different terms for parent's opposite sex sibling terms.	
Omaha	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate terms tend to be applied to relatives of the same generation who are linked to ego through connecting relatives of a different sex."	A uni-local residence rule brings into proximity a group of relatives linked under one line of decent. This rule acts as a social differential to support bifurcation of cousin terms.	Murdock, G. P. (1949). Social structure (Vol. xvii). Oxford, England: Macmillan.

Phylogenies

We tested hypotheses across three languages families, where data allowed. This was the Austronesian, Bantu, and Uto-Aztecan language phylogenies (Dunn et al., 2011; Gray et al., 2009; Grollemund et al., 2015). All language to phylogeny pairings were taken from decisions made in Kirby et al. (2016). In Austronesian, we sub-sampled 1000 phylogenies from a posterior sample of 4199 phylogenies. Austronesian phylogenies were estimated through linguistic data and supported by genetic evidence, and archaeological records. Detailed methods can be found in Gray et al. (2009). Trees were pruned from the original sample of 400 languages, to 80 languages based on data availability. In Bantu, we sampled 1000 from a posterior sample of 2000 phylogenies developed in Grollemund et al. (2015). These trees were built using linguistic data and calibrated using the archaeological record. Trees were pruned from the original sample of 425 languages, to 69 languages based on data availability. In Uto-Aztecan, we sampled 1000 phylogenies from a posterior of 10,000 phylogenies modeled by Dunn et al. (2011). This posterior was built using linguistic data. Trees were pruned from the original sample of 34 languages, to 19 based on data availability. All branch lengths are standardized to have a mean length of 0.1, as per BayesTraits recommendations.

Signal tests

We performed 4 signal tests to assess the hypotheses that shared-ancestry was a constraint on kinship diversity. The phylogenetic 'D' test uses simulation to determine whether the clustering of binary variables on a phylogeny follow patterns of Brownian motion (D = 0 indicates perfectly Brownian clusters and D < 0 strong clustering) or random clustering (D = 1 indicates complete randomness). To test whether geography may also predict the distribution of terminologies, we used Mantel tests. Mantel tests use random permutation and Pearson's correlation statistics to determine the correlation between two matrices. Here we compare log geographic distance, calculated with the Haversine formula, to a binary similarity matrix of each terminology present in each language family, each over the default setting of 999 permutations. To determine whether phylogenetic or geographic distances best determined the distribution of terminologies, we used partial Mantel tests. Partial Mantel tests control for a confounding third matrix, while comparing another two matrices. We perform a test between a terminology and geographic distance, controlling for phylogenetic distance, and another between terminology and phylogenetic distance, controlling for geographic distance. Phylogenetic distance is calculated using cophenetic distance, and the cophenetic function in R {stats} (R Core Team 2018). Table S4 shows the mean posterior result from 1000 phylogenies for all terminologies present within each language family. However, we only consider results viable if the terminology consists of more than 10% of the overall sample. All p-values are Bonferroni corrected.

The code for all signal tests can be found in file `analysis/signal-tests.R`. This file comes with helper functions `analysis/signal-functions` and `analysis/mantel-functions` for the D-statistic and Mantel tests respectively.

Table S4: Signal tests for each terminology within each language family. Columns 2 and 3 indicate the presence and absence of a terminology. Columns 4 to 6 are outputs from the D-statistic test. Columns 7 to 21 are output from Mantel tests. P-values and Bonferroni corrected values shown

	Terminology	Absent	Present	D	P. Brownian	P. Random	Z-stat	p-value	bonf-p	Z-stat	p-value	bonf-p	Z-stat	p-value	bonf-p	Statistic	p-value	bonf-p	Statistic	p-value	bonf-p
Austronesian	Crow	79	6	-0.115	0.603	0.036	1752616.53	0.039	0.233	3789.807	0.400	1.000	32.773	0.028	0.167	0.012	0.368	1.000	-0.116	0.977	1.000
	Eskimo	71	14	-0.494	0.806	0.000	4905208.29	0.219	1.000	8155.126	0.180	0.985	78.033	0.038	0.229	-0.004	0.500	1.000	0.133	0.031	0.184
	Hawaiian	37	48	0.661	0.054	0.081	8021595.70	0.959	1.000	14388.168	0.854	1.000	131.969	0.596	1.000	-0.001	0.446	1.000	-0.010	0.665	1.000
	Iroquois	70	15	0.097	0.468	0.007	4216334.11	0.032	0.190	8460.864	0.484	1.000	74.751	0.005	0.030	0.028	0.248	1.000	-0.125	0.997	1.000
	Omaha	84	1	2.860	0.230	0.700	430380.25	0.376	1.000	702.380	0.377	1.000	6.328	0.867	1.000	0.044	0.171	0.975	-0.014	0.626	1.000
	Sudanese	84	1	-2.063	0.714	0.171	498098.38	0.260	1.000	709.856	0.281	1.000	6.220	0.826	1.000	0.067	0.118	0.710	-0.035	0.674	1.000
Bantu	Crow	65	4	1.105	0.129	0.525	348598.29	0.887	1.000	1823.446	0.857	1.000	15359.566	0.627	1.000	-0.011	0.512	1.000	-0.063	0.670	1.000
	Descriptive	68	1	2.941	0.066	0.881	93014.64	0.783	1.000	477.297	0.900	1.000	5417.879	0.233	1.000	-0.031	0.603	1.000	0.136	0.077	0.537
	Hawaiian	60	9	0.405	0.297	0.083	792380.62	0.524	1.000	3835.774	0.496	1.000	35032.624	0.542	1.000	0.031	0.284	1.000	0.040	0.288	1.000
	Iroquois	25	44	0.166	0.362	0.008	1636008.46	0.023	0.159	7853.277	0.007	0.046	71119.715	0.151	0.892	0.105	0.005	0.038	0.051	0.138	0.863
	Mixed	68	1	-2.432	0.834	0.040	116322.82	0.320	1.000	500.446	0.290	1.000	3836.258	0.916	1.000	0.086	0.121	0.844	-0.067	0.854	1.000
	Omaha	61	8	0.767	0.140	0.274	733279.95	0.393	1.000	3484.320	0.309	1.000	32352.914	0.396	1.000	0.051	0.197	1.000	0.067	0.218	1.000
	Sudanese	67	2	1.051	0.287	0.459	169263.56	0.718	1.000	929.736	0.623	1.000	10075.747	0.223	1.000	-0.066	0.840	1.000	0.148	0.083	0.580
Uto-Aztecan	Crow	21	1	0.243	0.419	0.462	13195.12	0.365	1.000	132.056	0.998	1.000	0.025	0.659	0.990	-0.022	0.484	1.000	0.060	0.341	0.935
	Eskimo	21	1	3.253	0.216	0.679	14128.24	0.818	1.000	133.048	0.909	1.000	0.026	0.504	0.974	-0.003	0.355	1.000	0.087	0.255	0.827
	Hawaiian	6	16	-0.600	0.798	0.004	70096.07	0.259	0.980	606.534	0.596	1.000	0.114	0.136	0.545	-0.035	0.604	1.000	0.145	0.073	0.291
	Iroquois	18	4	-2.343	0.985	0.000	54649.14	0.881	1.000	457.499	0.973	1.000	0.086	0.235	0.840	0.001	0.438	1.000	0.134	0.120	0.479

Ancestral state

MCMC review

Ancestral state inference allows us to estimate the probability of a particular terminology at the root of each language phylogeny, as well as estimating the patterns of change between each state. We perform Bayesian reversible-jump MCMC ancestral state inference kinship terminologies using BayesTraits V 3.0 Multistate (Pagel and Meade 2017). Multistate uses a posterior of phylogenies to estimate the probability of each terminology present in the taxa at the phylogeny root, and an estimation of the rate (Q) matrix. The reversible-jump approach searches the model space for an optimal solution by dynamically setting some rate parameters (i.e. transitions from one state to another) to zero. This results in searching the model space where we are confident transition rates are non-zero. The Q matrix shows the likelihood of changing from any state to any other. MCMC chains were run for 10_9 iterations, sampling every 50,000 iterations with a burn-in of 10,000 iterations, to give a posterior sample of 20,000. Each analysis ran three times to test consistent MCMC convergence using the Gelman-Rubin diagnostic (Gelman and Rubin 1992). Due to uncertainty in the inference of the Bantu ancestral state, each terminology present in the phylogeny was 'fossilized' as the root to estimate likelihoods. Effectively, this forces the algorithm to build a model given a particular ancestral state and given the contemporary data. We can then compare the model fit across each constrained model. We calculate pairwise Bayes factors (BF) to assess the evidence for each response. BF < 3 indicates weak evidence, >3 positive evidence, and >10 very strong evidence. This is shown in section 3.1.1.

Table S5: Three MCMC chains for the Austronesian language family. The base probability for any type is 0.167.

	Lh	Crow	Eskimo	Hawaiian	Iroquois	Omaha	Sudanese
1	-95.053	0.029	0.846	0.011	0.015	0.042	0.057
2	-95.037	0.029	0.846	0.010	0.015	0.042	0.058
3	-95.042	0.029	0.848	0.010	0.014	0.041	0.057
Mean	-95.044	0.029	0.847	0.010	0.015	0.042	0.057

Table S6: Three MCMC chains for the Bantu language family. The base probability for any type is 0.143.

	Lh	Crow	Descriptive	Hawaiian	Iroquois	Omaha	Sudanese	Mixed
1	-81.151	0.089	0.078	0.157	0.393	0.101	0.082	0.099
2	-81.134	0.090	0.078	0.156	0.395	0.102	0.081	0.097
3	-81.141	0.089	0.078	0.156	0.397	0.101	0.081	0.098
Mean	-81.142	0.089	0.078	0.156	0.395	0.101	0.081	0.098

Table S7: Three MCMC chains for the Uto-Aztecan language family. The base probability for any type is 0.25.

	Lh	Crow	Eskimo	Hawaiian	Iroquois
1	-19.279	0.232	0.226	0.310	0.232
2	-19.291	0.232	0.224	0.312	0.232
3	-19.282	0.232	0.225	0.311	0.232
Mean	-19.284	0.232	0.225	0.311	0.232

Table S8: Gelman-Rubin tests of MCMC convergence for each language family

	Point est.	Upper C.I.
austronesian	1	1
bantu	1	1
Uto-Aztecan	1	1

Fossilized Bantu

MCMC Review

We fossilize the ancestral state for each possible terminology within Bantu in an attempt to determine the most plausible ancestral state. Below are the marginal log-likelihoods for these models and the result with comparisons to the most likely ancestral state, Iroquoian.

Table S9: Marginal log-likelihood for each fossilized terminology in Bantu

terminology	MLL
Crow	-91.683
Descriptive	-90.914
Hawaiian	-91.450
Iroquois	-90.297
Mixed	-91.819
Omaha	-90.805
Sudanese	-92.595

Bayes factor model comparison

Bayes factor calculations show that there is some evidence for an Iroquoian root over a Hawaiian root (BF = 2.306). The table below shows comparisons to the fossilized Iroquois root to all other fossilized roots.

Table S10: Pairwise Bayes factor between Iroquois and all other possible states.

terminology	Bayes' Factor
Crow	2.772
Descriptive	1.235
Hawaiian	2.306
Iroquois	0.000
Mixed	3.043
Omaha	1.017
Sudanese	4.595

Fossilized Uto-Aztecan

MCMC Review

As with Bantu, we fossilize the ancestral state for each possible terminology within Uto-Aztecan to determine the most plausible ancestral state. Below are the Bayes Factor comparisons between the most likely ancestral state & all other possible states. There is no preference for a particular ancestral state.

Table S12: Pairwise Bayes factor between Hawaiian and all other possible states.

terminology	Bayes' Factor
Crow	-0.103
Eskimo	0.058
Hawaiian	0.000
Iroquois	0.852

PMP in Austronesia

Here we reconstruct the PMP state in Austronesian using the RecNode command in BayesTraits. All other settings remain the same as the Austronesian model.

Table S13: Ancestral state for PMP

	Probability
RecNode P(1)	0.020
RecNode P(3)	0.897
RecNode P(4)	0.004
RecNode P(5)	0.006
RecNode P(6)	0.026
RecNode P(7)	0.046

Transition rates

RJ ancestral state analysis also estimates the rate of transition between kinship terminological types. The model constrains the number of parameters estimated, forcing some parameters to be zero, and then estimates and appropriate number of parameters for accurately represent the model. By looking at which parameters are set to zero across the MCMC chain, and comparing that with the number of times we would expect a transition to be estimated under the priors of the model we can see which transition rates the model believes to be important (Currie et al., 2010). We assume that if the posterior-to-prior odds are less than one, we have no evidence to support a particular transition being zero (*italicized rows have prior-posterior odds less than 1*).

Table S14: Transition rates between kin terminologies in the Austronesian language family.

transition	parameterized	zero	percentage	posterior-prior odds
Crow -> Hawaiian	*9160*	*840*	*0.916*	*0.349*
Eskimo -> Hawaiian	*9080*	*920*	*0.908*	*0.386*
Hawaiian -> Iroquois	*8921*	*1079*	*0.892*	*0.461*
Omaha -> Hawaiian	7260	2740	0.726	1.438
Sudanese -> Hawaiian	7114	2886	0.711	1.545
Iroquois -> Hawaiian	6993	3007	0.699	1.638
Omaha -> Crow	6919	3081	0.692	1.696
Crow -> Iroquois	6792	3208	0.679	1.799
Omaha -> Sudanese	6561	3439	0.656	1.997
Crow -> Omaha	6499	3501	0.650	2.052
Omaha -> Iroquois	6436	3564	0.644	2.110
Sudanese -> Crow	6305	3695	0.631	2.233
Iroquois -> Crow	6270	3730	0.627	2.266
Sudanese -> Omaha	6128	3872	0.613	2.407
Crow -> Sudanese	5964	4036	0.596	2.578
Sudanese -> Iroquois	5875	4125	0.588	2.675
Hawaiian -> Crow	5622	4378	0.562	2.967
Sudanese -> Eskimo	4980	5020	0.498	3.840
Omaha -> Eskimo	4876	5124	0.488	4.003
Iroquois -> Omaha	4191	5809	0.419	5.280
Crow -> Eskimo	3699	6301	0.370	6.489
Iroquois -> Sudanese	3229	6771	0.323	7.988
Eskimo -> Sudanese	2182	7818	0.218	13.649
Hawaiian -> Omaha	1851	8149	0.185	16.771
Hawaiian -> Sudanese	1279	8721	0.128	25.976
Eskimo -> Crow	1005	8995	0.101	34.096
Eskimo -> Omaha	953	9047	0.095	36.165

Iroquois -> Eskimo	846	9154	0.085	41.221
Eskimo -> Iroquois	410	9590	0.041	89.106
Hawaiian -> Eskimo	255	9745	0.025	145.584

Table S15: Transition rates between kin terminologies in the Bantu language family.

transition	parameterized	zero	percentage	posterior-prior odds
Iroquois -> Omaha	*9163*	*837*	*0.916*	*0.420*
Iroquois -> Hawaiian	8137	1863	0.814	1.053
Omaha -> Descriptive	7956	2044	0.796	1.182
Crow -> Sudanese	7449	2551	0.745	1.575
Omaha -> Iroquois	7339	2661	0.734	1.668
Sudanese -> Crow	6938	3062	0.694	2.030
Crow -> Hawaiian	6928	3072	0.693	2.040
Hawaiian -> Crow	6716	3284	0.672	2.249
Omaha -> Hawaiian	6447	3553	0.645	2.535
Crow -> Iroquois	6390	3610	0.639	2.599
Sudanese -> Hawaiian	6330	3670	0.633	2.667
Omaha -> Crow	6181	3819	0.618	2.842
Descriptive -> Omaha	6119	3881	0.612	2.917
Omaha -> Sudanese	5996	4004	0.600	3.072
Hawaiian -> Iroquois	5875	4125	0.588	3.229
Descriptive -> Hawaiian	5834	4166	0.583	3.285
Sudanese -> Omaha	5834	4166	0.583	3.285
Mixed -> Hawaiian	5722	4278	0.572	3.439
Sudanese -> Iroquois	5716	4284	0.572	3.447
Descriptive -> Crow	5576	4424	0.558	3.649
Crow -> Omaha	5546	4454	0.555	3.694
Mixed -> Omaha	5517	4483	0.552	3.738
Mixed -> Crow	5441	4559	0.544	3.854
Descriptive -> Mixed	5430	4570	0.543	3.871
Sudanese -> Mixed	5424	4576	0.542	3.880
Omaha -> Mixed	5417	4583	0.542	3.891
Mixed -> Iroquois	5411	4589	0.541	3.901
Crow -> Mixed	5362	4638	0.536	3.979
Descriptive -> Sudanese	5292	4708	0.529	4.092
Descriptive -> Iroquois	5280	4720	0.528	4.112
Sudanese -> Descriptive	5222	4778	0.522	4.209
Mixed -> Sudanese	5086	4914	0.509	4.444
Iroquois -> Crow	5075	4925	0.508	4.464

Mixed -> Descriptive	4959	5041	0.496	4.676
Crow -> Descriptive	4762	5238	0.476	5.059
Hawaiian -> Omaha	4197	5803	0.420	6.360
Hawaiian -> Sudanese	4080	5920	0.408	6.674
Hawaiian -> Mixed	3473	6527	0.347	8.644
Hawaiian -> Descriptive	2656	7344	0.266	12.718
Iroquois -> Sudanese	1774	8226	0.177	21.328
Iroquois -> Mixed	379	9621	0.038	116.762
Iroquois -> Descriptive	208	9792	0.021	216.534

Table S16: Transition rates between kin terminologies in the Uto-Aztecan language family.

transition	parameterized	zero	percentage	posterior-prior odds
Iroquois -> Hawaiian	*9511*	*489*	*0.951*	*0.123*
Crow -> Hawaiian	*8658*	*1342*	*0.866*	*0.371*
Eskimo -> Hawaiian	*8393*	*1607*	*0.839*	*0.459*
Hawaiian -> Iroquois	*8036*	*1964*	*0.804*	*0.585*
Eskimo -> Iroquois	*7254*	*2746*	*0.725*	*0.907*
Crow -> Iroquois	*7220*	*2780*	*0.722*	*0.922*
Crow -> Eskimo	6975	3025	0.698	1.039
Iroquois -> Eskimo	6877	3123	0.688	1.088
Eskimo -> Crow	6736	3264	0.674	1.160
Iroquois -> Crow	6240	3760	0.624	1.443
Hawaiian -> Crow	1380	8620	0.138	14.960
Hawaiian -> Eskimo	1336	8664	0.134	15.531

Guillon and Mace comparison

Previous research performed by Guillon and Mace in, using similar methods, found support for a Hawaiian root, with some evidence of an Iroquoian root within the Bantu language family. The numerical results for this analysis are not available in the paper. This is the inverse of our result, which found most support for an Iroquoian root, with some support for Hawaiian. This discrepancy is concerning considering the terminological data for both analyses come from D-PLACE. The primary difference between approaches is that here we use Grollemund et al. (2015) more recently developed phylogeny (against Currie et al. (2014)), and secondarily, Guillon and Mace include missing data, where we exclude it. We re-analysed our data including missing data and found no change in our previous conclusions. Suggesting that the improved phylogeny is driving the change in results.

Table S17: Ancestral state of Bantu with missing data included

	probability
Crow	0.124
Descriptive	0.117
Hawaiian	0.139
Iroquois	0.259
Omaha	0.124
Sudanese	0.119
Mixed	0.118

Co-evolution tests

MCMC settings

All co-evolutionary analyses was performed in BayesTraits v3.1 using Discrete models (M. Pagel & Meade, 2017). For all models we used a Reversible Jump MCMC approach and tested an independent and dependent model of evolution. In an independent model, a trait can change, regardless of the state of the other trait. In a dependent model, a trait change is dependent on the state of the second trait. If co-evolution has occurred, the data should fit a dependent model better than it fits an independent model. We test this using Bayes Factors and the same guides as described previously in the paper and SM. Analyses were run between 10,010,000 and 65,000,000 iterations, with burn-ins ranging between 10,000 and 55,000,000, and sampling every 1000 iterations. The results are a posterior of 10,000 iterations, approximately 10 iterations per tree per hypotheses. A stepping stone sampler was used to estimate the marginal likelihood. We used 100 stones sampled every 1,000 iterations. For details of the prior and other settings for each hypothesis, see the table below.

Table S18: MCMC settings for both dependent and independent analyses

hypotheses	exp. mean	scaled branch length	iterations	sampling	burn-in	posterior size
austronesian-crow-high.polygyny	10	Yes	10050000	1000	50000	10000
austronesian-crow-matri.anvunclocalresidence	10	Yes	10050000	1000	50000	10000
austronesian-crow-matrilineal	10	Yes	10050000	1000	50000	10000
austronesian-crow-polygyny	10	Yes	10050000	1000	50000	10000
austronesian-crow-matrilocal	10	Yes	10010000	1000	10000	10000
austronesian-crow-matrilocal.strict	10	Yes	10010000	1000	10000	10000
austronesian-crow-uni.localresidence	10	Yes	10010000	1000	10000	10000
austronesian-eskimo-absenceofcousinmarriage.permitted	10	Yes	65000000	1000	55000000	10000
austronesian-eskimo-absenceofcousinmarriage.preference	10	Yes	65000000	1000	55000000	10000
austronesian-eskimo-bi.linealdescent	10	Yes	10010000	1000	10000	10000
austronesian-eskimo-monogamy	10	Yes	10050000	1000	50000	10000
austronesian-eskimo-neo.localresidence	10	Yes	65000000	1000	55000000	10000
austronesian-eskimo-nuclear.families	10	Yes	10010000	1000	10000	10000
austronesian-eskimo-uni.linealdescent	10	Yes	10010000	1000	10000	10000
austronesian-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10050000	1000	50000	10000
austronesian-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1000	10000	10000
austronesian-hawaiian-bi.linealdescent	10	Yes	10010000	1000	10000	10000
austronesian-hawaiian-bi.localextendedfamily	10	Yes	10010000	1000	10000	10000
austronesian-hawaiian-bi.localresidence	10	Yes	10050000	1000	50000	10000

austronesian-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-exogamy.unilineal.descent	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-high.polygyny	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-matri.anvunclocalresidence	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-polygyny	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-uni.linealdescent	10	Yes	10010000	1000	10000	10000
austronesian-iroquois-uni.localresidence	10	Yes	10050000	1000	50000	10000
bantu-crow-matri.anvunclocalresidence	10	Yes	10010000	1000	10000	10000
bantu-crow-matrilineal	10	Yes	10010000	1000	10000	10000
bantu-crow-matrilocal	10	Yes	10050000	1000	50000	10000
bantu-crow-matrilocal.strict	10	Yes	10050000	1000	50000	10000
bantu-crow-uni.localresidence	10	Yes	10010000	1000	10000	10000
bantu-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	1000	10000	10000
bantu-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1000	10000	10000
bantu-hawaiian-bi.linealdescent	10	Yes	10010000	1000	10000	10000
bantu-hawaiian-bi.localextendedfamily	10	Yes	10010000	1000	10000	10000
bantu-hawaiian-bi.localresidence	10	Yes	10010000	1000	10000	10000
bantu-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	1000	10000	10000
bantu-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1000	10000	10000
bantu-iroquois-exogamy.unilineal.descent	10	Yes	10010000	1000	10000	10000
bantu-iroquois-matri.anvunclocalresidence	10	Yes	10010000	1000	10000	10000
bantu-iroquois-uni.linealdescent	10	Yes	10010000	1000	10000	10000
bantu-iroquois-uni.localresidence	10	Yes	10010000	1000	10000	10000
bantu-omaha-matri.anvunclocalresidence	10	Yes	10010000	1000	10000	10000
bantu-omaha-patrilineal	10	Yes	10010000	1000	10000	10000
bantu-omaha-patrilocal	10	Yes	10010000	1000	10000	10000
bantu-omaha-patrilocal.strict	10	Yes	10010000	1000	10000	10000
bantu-omaha-uni.localresidence	10	Yes	10010000	1000	10000	10000
uto-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	1000	10000	10000
uto-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	1000	10000	10000
uto-hawaiian-bi.linealdescent	10	Yes	10010000	1000	10000	10000
uto-hawaiian-bi.localextendedfamily	10	Yes	10010000	1000	10000	10000
uto-hawaiian-bi.localresidence	10	Yes	10010000	1000	10000	10000
uto-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	1000	10000	10000
uto-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	1000	10000	10000

uto-iroquois-exogamy.unilineal.descent	10	Yes	10010000	1000	10000	10000
uto-iroquois-high.polygyny	10	Yes	10010000	1000	10000	10000
uto-iroquois-matri.anvunclocalresidence	10	Yes	10010000	1000	10000	10000
uto-iroquois-uni.linealdescent	10	Yes	10010000	1000	10000	10000
uto-iroquois-uni.localresidence	10	Yes	10010000	1000	10000	10000

MCMC review and Bayes Factors

Here we show the results of MCMC chains and respective tests. The first table for each hypothesis is a review of the MCMC chains. Each row shows the marginal log-likelihood and averaged transition rates for the dependent and independent models for a single chain. There are three MCMC chains run for each hypothesis to ensure the model is reaching the same conclusion each time. The penultimate row shows the mean across the three runs. The final row tests which model was more appropriate for the data. We calculate a Bayes-factor, which compares the log marginal likelihood between the dependent and independent models, as explained in Pagel & Meade (2006). A Bayes Factor greater than ten indicates strong support, greater than three positive support and less than three no support.

A second table shows the results of a Gelman-Rubin diagnostic testing, to test for any significant differences between chains (Gelman & Rubin, 1992). A value of 1 indicates no difference, and a rule of thumb suggests point-estimates of less than 1.1 indicate negligible differences between chains.

Some extra analyses are also shown here that are not seen in table 1. These are matrilocal and patrilocal hypotheses and matrilocal.strict and patrilocal.strict. The strict hypothesis excludes anything, but societies classified as patrilocal or matrilocal. In the main text we discuss the differences between including virilocality and uxorilocality under each of these hypotheses, there are represented in the 'not strict' hypothesis.

Table S19: Austronesian : Crow <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-58.486	2.537	1.219	17.085	2.878	23.205	4.089	7.454	6.586	-59.016	1.68	21.444	2.778	15.975
2	-58.607	2.521	1.259	16.807	2.979	23.77	4.074	7.654	6.568	-58.942	1.704	21.656	2.777	15.799
3	-58.54	2.546	1.236	17.188	2.985	23.439	4.042	7.67	6.556	-59.1	1.688	21.731	2.827	16.154
Mean	-58.544	2.535	1.238	17.027	2.947	23.471	4.068	7.593	6.57	-59.019	1.691	21.61	2.794	15.976
BF	1.059													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S20: Austronesian : Crow <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-54.688	0.997	0.367	6.689	8.886	12.439	10.346	17.49	4.623	-59.875	1.604	21.99	1.166	5.64
2	-54.6	1.007	0.348	6.647	8.906	12.272	9.917	17.536	4.619	-60.003	1.622	22.299	1.165	5.674
3	-54.71	0.991	0.366	6.628	8.98	12.309	10.322	17.464	4.705	-59.84	1.609	21.951	1.165	5.626
Mean	-54.666	0.998	0.36	6.655	8.924	12.34	10.195	17.497	4.649	-59.906	1.612	22.08	1.165	5.647
BF	10.374													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S21: Austronesian : Crow <-> Matrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-55.963	0.755	0.324	5.045	8.59	12.393	11.438	17.922	8.894	-61.187	1.573	21.589	1.01	6.265
2	-56.018	0.765	0.318	5.079	8.606	12.566	11.038	17.838	8.997	-61.205	1.575	21.477	1	6.224
3	-56.128	0.751	0.322	5.082	8.556	12.417	11.061	17.805	8.803	-61.206	1.574	21.449	1.003	6.315
Mean	-56.036	0.757	0.321	5.069	8.584	12.459	11.179	17.855	8.898	-61.199	1.574	21.505	1.004	6.268
BF	10.45													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S22: Austronesian : Crow <-> Polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-68.567	2.689	2.512	1.505	0.917	24.339	6.913	9.728	4.795	-67.647	1.657	21.326	2.6	1.569
2	-68.762	2.715	2.488	1.519	0.922	24.556	6.997	9.912	4.883	-67.63	1.659	21.246	2.606	1.566
3	-68.648	2.711	2.553	1.529	0.921	24.159	6.962	9.776	4.906	-67.461	1.661	21.217	2.652	1.576
Mean	-68.659	2.705	2.518	1.518	0.92	24.351	6.957	9.805	4.861	-67.579	1.659	21.263	2.619	1.57
BF	-1.839													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S23: Austronesian : Crow <-> Matrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-52.623	0.781	0.535	6.674	7.172	9.728	4.808	19.083	6.265	-53.849	1.553	20.979	0.787	5.359
2	-52.695	0.766	0.551	6.503	7.071	9.989	4.887	18.722	6.404	-53.885	1.554	21.072	0.777	5.377
3	-52.637	0.781	0.555	6.751	7.007	9.774	5.053	18.934	6.29	-53.889	1.545	21.074	0.781	5.354
Mean	-52.652	0.776	0.547	6.643	7.083	9.83	4.916	18.913	6.32	-53.874	1.551	21.042	0.782	5.363
BF	2.452													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S24: Austronesian : Crow <-> Matrilocal.strict

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-46.668	0.472	0.528	5.731	8.376	9.268	4.732	18.061	5.755	-48.368	1.524	20.319	0.5	4.531
2	-46.868	0.473	0.539	5.714	8.355	9.402	4.752	18.237	5.754	-48.467	1.48	20.299	0.506	4.565
3	-46.751	0.474	0.528	5.738	8.262	9.218	4.623	18.336	5.835	-48.524	1.51	20.168	0.501	4.466
Mean	-46.762	0.473	0.532	5.728	8.331	9.296	4.702	18.211	5.781	-48.453	1.505	20.262	0.502	4.521
BF	3.401													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S25: Austronesian : Crow <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-72.461	1.442	0.316	2.925	4.261	14.85	10.992	20.857	2.46	-74.574	1.325	17.603	1.477	2.675
2	-72.68	1.466	0.318	2.9	4.179	15.043	10.985	20.603	2.418	-74.309	1.311	17.577	1.496	2.682
3	-72.343	1.459	0.322	2.924	4.109	14.996	11.26	20.652	2.414	-74.434	1.312	17.239	1.493	2.693
Mean	-72.495	1.456	0.319	2.916	4.183	14.963	11.079	20.704	2.431	-74.439	1.316	17.473	1.489	2.683
BF	4.228													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S26: Austronesian : Eskimo <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-79.717	14.908	1.986	3.834	0.336	5.256	7.162	3.325	5.801	-79.556	0.252	3.432	14.372	5.077
2	-79.605	15.275	1.965	3.9	0.329	5.323	7.195	3.27	5.932	-79.494	0.251	3.422	14.448	5.046
3	-79.732	14.862	1.948	3.843	0.349	5.299	7.131	3.281	5.823	-79.556	0.262	3.431	14.551	5.053
Mean	-79.685	15.015	1.966	3.859	0.338	5.293	7.163	3.292	5.852	-79.535	0.255	3.428	14.457	5.059
BF	-0.323													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.002

Table S27: Austronesian : Eskimo <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-70.961	4.325	0.376	18.722	1.117	3.242	0.926	11.685	13.576	-69.75	0.252	3.443	3.733	20.012
2	-70.936	4.356	0.38	18.774	1.126	3.254	0.945	11.431	13.434	-69.81	0.251	3.451	3.748	19.94
3	-70.597	4.356	0.382	18.867	1.106	3.226	0.91	11.764	13.332	-69.799	0.26	3.458	3.689	19.721
Mean	-70.831	4.346	0.379	18.788	1.116	3.241	0.927	11.627	13.447	-69.786	0.254	3.451	3.723	19.891
BF	-2.423													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.000

Table S28: Austronesian : Eskimo <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-92.099	4.625	0.685	5.322	0.5	3.896	1.499	5.741	9.434	-91.281	0.165	3.213	2.651	4.338
2	-92.021	4.655	0.661	5.433	0.506	3.879	1.526	5.903	9.614	-91.134	0.167	3.199	2.645	4.319
3	-91.91	4.65	0.666	5.415	0.495	3.879	1.521	5.832	9.371	-91.503	0.161	3.183	2.619	4.302
Mean	-92.01	4.643	0.671	5.39	0.5	3.885	1.515	5.825	9.473	-91.306	0.164	3.198	2.638	4.32
BF	-1.634													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S29: Austronesian : Eskimo <-> Monogamy

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-70.882	0.964	0.331	3.596	5.71	4.521	9.368	5.121	5.901	-74.566	0.188	3.145	1.265	2.361
2	-70.993	0.956	0.322	3.639	5.569	4.46	9.625	5.075	6.011	-74.593	0.187	3.174	1.269	2.382
3	-71.014	0.95	0.33	3.561	5.553	4.473	9.491	5.016	6.031	-74.514	0.185	3.18	1.275	2.41
Mean	-70.963	0.957	0.328	3.599	5.611	4.485	9.495	5.071	5.981	-74.558	0.187	3.166	1.27	2.384
BF	7.368													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S30: Austronesian : Eskimo <-> Neo.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-52.993	0.19	0.207	8.934	10.115	3.249	4.742	6.91	11.153	-56.985	0.166	3.223	0.619	7.221
2	-52.876	0.188	0.205	8.96	10.336	3.262	4.683	6.987	10.939	-56.776	0.169	3.241	0.618	7.133
3	-52.852	0.189	0.202	8.97	10.232	3.233	4.714	6.961	11.16	-56.722	0.165	3.214	0.619	7.184
Mean	-52.907	0.189	0.205	8.955	10.228	3.248	4.713	6.953	11.084	-56.828	0.167	3.226	0.619	7.179
BF	7.984													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.001	1.002

Table S31: Austronesian : Eskimo <-> Nuclear.families

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-88.88	4.445	0.542	6.428	1.792	7.766	10.399	4.003	3.262	-89.35	0.17	3.154	3.983	4.046
2	-89.04	4.413	0.539	6.373	1.827	7.626	10.282	4.013	3.18	-89.26	0.167	3.167	3.965	4.042
3	-88.89	4.394	0.531	6.483	1.735	7.539	10.413	4.001	3.202	-89.11	0.17	3.169	3.954	4.029
Mean	-88.93	4.417	0.537	6.428	1.785	7.644	10.365	4.006	3.215	-89.24	0.169	3.163	3.967	4.039
BF	0.963													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

Table S32: Austronesian : Eskimo <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-86.068	2.3	0.518	3.44	0.558	3.108	1.524	11.284	10.553	-85.802	0.179	3.218	1.437	3.442
2	-86.834	2.335	0.507	3.427	0.553	3.098	1.531	11.294	10.388	-85.815	0.188	3.228	1.443	3.433
3	-86.23	2.326	0.515	3.428	0.562	3.142	1.5	11.261	10.464	-85.894	0.178	3.249	1.489	3.432
Mean	-86.377	2.32	0.513	3.432	0.558	3.116	1.518	11.28	10.468	-85.837	0.182	3.232	1.456	3.436
BF	-0.532													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S33: Austronesian : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-102.542	4.757	4.315	2.359	8.871	4.497	15.427	7.638	4.567	-102.648	6.738	6.067	14.573	5.101
2	-102.493	4.618	4.2	2.318	8.747	4.58	15.457	7.478	4.706	-102.624	6.728	6.057	14.533	5.056
3	-102.484	4.928	4.295	2.318	8.716	4.681	15.472	7.413	4.679	-102.653	6.714	6.118	14.56	5.082
Mean	-102.506	4.768	4.27	2.332	8.778	4.586	15.452	7.51	4.651	-102.642	6.727	6.081	14.555	5.08
BF	0.211													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S34: Austronesian : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-90.287	5.743	8.441	15.65	3.337	5.406	1.791	15.294	18.575	-92.997	6.826	6.077	3.729	19.744
2	-90.123	5.701	8.469	15.488	3.263	5.415	1.751	14.794	18.612	-92.902	6.923	6.194	3.669	19.448
3	-90.152	5.76	8.46	15.71	3.36	5.442	1.798	14.817	18.572	-92.962	6.762	6.043	3.688	19.664
Mean	-90.187	5.735	8.457	15.616	3.32	5.421	1.78	14.968	18.586	-92.954	6.837	6.105	3.695	19.619
BF	5.421													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S35: Austronesian : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-111.998	4.097	10.549	13.825	8.256	16.902	3.161	2.369	3.754	-117.348	7.679	6.872	2.454	4.274
2	-111.94	4.077	10.469	13.909	8.299	16.719	3.226	2.428	3.772	-117.297	7.696	6.824	2.461	4.253
3	-111.932	4.107	10.525	13.756	8.355	16.86	3.097	2.39	3.732	-117.44	7.782	6.855	2.451	4.272
Mean	-111.957	4.094	10.514	13.83	8.303	16.827	3.161	2.396	3.753	-117.362	7.719	6.85	2.455	4.266
BF	10.7													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S36: Austronesian : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-114.384	3.253	5.948	4.958	15.829	8.111	5.442	7.51	5.988	-114.856	8.786	7.252	3.461	4.918
2	-114.362	3.262	5.96	4.986	16.21	8.028	5.454	7.715	6.009	-114.884	8.792	7.195	3.441	4.841
3	-114.248	3.215	5.943	5.035	15.987	8.004	5.456	7.63	5.996	-114.913	8.761	7.25	3.485	4.868
Mean	-114.331	3.243	5.95	4.993	16.009	8.048	5.451	7.618	5.998	-114.884	8.78	7.232	3.462	4.876
BF	0.945													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.002

Table S37: Austronesian : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-103.861	3.23	7.307	14.812	7.149	6.874	5.444	4.684	19.514	-103.088	7.012	6.119	5.049	20.602
2	-103.682	3.213	7.346	14.382	6.961	6.89	5.482	4.642	19.89	-102.992	6.974	6.097	5.003	20.464
3	-103.945	3.177	7.468	14.755	7.139	6.911	5.493	4.843	19.925	-102.963	6.898	6.031	4.964	20.284
Mean	-103.829	3.207	7.374	14.65	7.083	6.892	5.473	4.723	19.776	-103.014	6.961	6.082	5.005	20.45
BF	-1.547													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S38: Austronesian : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-66.212	2.049	0.825	22.418	11.112	6.292	5.084	5.625	10.023	-70.779	1.55	5.952	3.082	20.328
2	-66.078	2.035	0.809	22.079	11.321	6.317	5.223	5.484	10.178	-70.666	1.526	5.964	3.063	20.467
3	-66.007	2.039	0.806	22.48	11.465	6.273	5.088	5.678	9.919	-70.674	1.535	5.856	3.065	20.308
Mean	-66.099	2.041	0.813	22.326	11.299	6.294	5.132	5.596	10.04	-70.706	1.537	5.924	3.07	20.368
BF	9.135													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S39: Austronesian : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-89.481	7.937	0.769	14.233	3.791	10.733	12.362	6.278	2.794	-94.37	1.526	5.851	9.951	11.869
2	-89.475	7.963	0.792	14.414	3.715	10.917	12.374	6.15	2.8	-94.26	1.524	5.854	10.026	12.15
3	-89.216	7.93	0.795	14.286	3.696	10.931	12.209	6.159	2.797	-94.27	1.509	5.798	10.106	12.134
Mean	-89.391	7.943	0.785	14.311	3.734	10.86	12.315	6.196	2.797	-94.3	1.52	5.834	10.028	12.051
BF	9.785													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S40: Austronesian : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-53.48	0.896	1.035	16.672	8.804	5.495	2.883	5.831	15.25	-53.582	1.143	5.231	1.199	18.629
2	-53.262	0.876	1.037	16.762	8.615	5.446	2.896	5.71	15.16	-53.591	1.131	5.157	1.189	18.488
3	-53.163	0.882	1.019	16.582	8.725	5.46	2.866	5.695	14.919	-53.578	1.122	5.166	1.193	18.442
Mean	-53.302	0.885	1.03	16.672	8.715	5.467	2.882	5.745	15.11	-53.584	1.132	5.185	1.194	18.52
BF	0.205													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S41: Austronesian : Iroquois <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-67.953	2.031	1.149	15.69	6.505	7.702	5.548	8.159	10.349	-69.217	1.711	7.769	2.754	15.809
2	-67.932	2.021	1.172	15.766	6.534	7.687	5.453	8.273	10.587	-69.048	1.701	7.852	2.806	16.062
3	-67.949	2.061	1.179	16.003	6.545	7.741	5.423	8.483	10.216	-69.301	1.698	7.807	2.753	15.811
Mean	-67.945	2.038	1.167	15.82	6.528	7.71	5.475	8.305	10.384	-69.189	1.703	7.809	2.771	15.894
BF	2.528													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S42: Austronesian : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-73.87	1.383	0.844	7.123	3.16	4.147	1.605	11.378	8.102	-72.25	1.045	4.985	1.153	5.678
2	-73.80	1.4	0.841	7.184	3.167	4.198	1.606	11.468	8.018	-72.407	1.055	5.016	1.166	5.737
3	-73.70	1.39	0.856	7.093	3.163	4.189	1.608	11.213	8.029	-72.18	1.049	4.976	1.16	5.625
Mean	-73.79	1.391	0.847	7.133	3.163	4.178	1.606	11.353	8.05	-72.279	1.05	4.992	1.16	5.68
BF	-3.243													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S43: Austronesian : Iroquois <-> Polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-78.608	1.915	1.063	1.325	2.521	11.089	11.082	9.884	3.903	-77.895	1.695	7.788	2.586	1.562
2	-78.508	1.919	1.061	1.331	2.566	10.846	11.184	10.011	3.916	-77.924	1.708	7.843	2.628	1.561
3	-78.393	1.914	1.078	1.328	2.6	10.918	11.112	10.047	3.865	-77.762	1.69	7.83	2.611	1.571
Mean	-78.503	1.916	1.067	1.328	2.562	10.951	11.126	9.981	3.895	-77.86	1.698	7.82	2.608	1.565
BF	-1.425													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.001
Independent	1.000	1.000

Table S44: Austronesian : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-87.18	0.937	0.834	4.408	5.463	6.662	10.617	9.374	4.777	-90.726	1.502	6.014	1.055	3.397
2	-87.37	0.934	0.827	4.447	5.421	6.419	10.811	9.27	4.666	-90.821	1.492	5.929	1.095	3.389
3	-87.08	0.936	0.829	4.423	5.524	6.446	10.838	9.442	4.75	-90.937	1.518	6	1.07	3.398
Mean	87.21	0.936	0.83	4.426	5.469	6.509	10.755	9.362	4.731	-90.828	1.504	5.981	1.073	3.395
BF	7.101													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S45: Austronesian : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-84.078	1.539	0.424	3.218	5.365	8.071	6.828	9.224	2.713	-87.299	1.046	5.167	1.408	2.469
2	-83.976	1.563	0.427	3.229	5.295	8.036	6.488	9.061	2.638	-87.331	1.054	5.161	1.408	2.485
3	-83.984	1.548	0.423	3.243	5.295	8.168	6.755	9.119	2.728	-87.242	1.03	5.111	1.393	2.483
Mean	-84.013	1.55	0.425	3.23	5.318	8.092	6.69	9.135	2.693	-87.291	1.043	5.146	1.403	2.479
BF	6.441													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S46: Bantu : Crow <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-63.233	3.683	0.933	8.457	2.134	16.453	7.622	14.886	7.657	-62.465	1.269	17.921	4.049	8.668
2	-63.222	3.759	0.931	8.619	2.118	15.965	7.62	14.76	7.5	-62.369	1.267	17.875	4.082	8.768
3	-63.23	3.744	0.936	8.622	2.106	16.082	7.723	14.656	7.519	-62.411	1.308	18.338	4.028	8.593
Mean	-63.228	3.729	0.933	8.566	2.119	16.167	7.655	14.767	7.559	-62.415	1.281	18.045	4.053	8.676
BF	-1.536													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S47: Bantu : Crow <-> Matrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-63.159	2.092	1.131	3.989	1.792	16.983	7.885	15.932	7.459	-62.249	1.276	18.031	2.289	4.109
2	-63.343	2.107	1.11	3.97	1.804	17.001	7.864	15.723	7.361	-62.244	1.293	18.128	2.326	4.177
3	-63.289	2.124	1.132	3.955	1.791	17.093	7.848	15.781	7.493	-62.241	1.272	17.898	2.276	4.119
Mean	-63.264	2.108	1.124	3.971	1.796	17.026	7.866	15.812	7.438	-62.245	1.28	18.019	2.297	4.135
BF	-1.82													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S48: Bantu : Crow <-> Matrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-36.08	0.844	0.861	15.206	5.526	15.506	5.245	11.085	11.464	-36.34	1.275	17.931	1.203	16.955
2	-35.87	0.849	0.903	15.359	5.536	16.053	5.295	11.284	11.188	-36.25	1.268	17.936	1.197	16.809
3	-35.96	0.868	0.878	15.47	5.526	15.841	5.241	11.172	11.245	-36.28	1.254	17.755	1.195	16.949
Mean	-35.97	0.854	0.881	15.345	5.529	15.8	5.26	11.18	11.299	-36.29	1.266	17.874	1.198	16.904
BF	0.523													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S49: Bantu : Crow <-> Matrilocal.strict

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-36.04	0.86	0.861	15.297	5.524	15.811	5.204	11.074	11.242	-36.42	1.258	17.746	1.198	16.758
2	-35.91	0.861	0.862	15.371	5.578	15.86	5.285	11.54	11.216	-36.36	1.271	17.976	1.18	16.774
3	-36.16	0.897	0.875	15.562	5.606	15.799	5.05	11.536	11.234	-36.31	1.255	18.041	1.191	16.829
Mean	-36.03	0.873	0.866	15.41	5.569	15.823	5.18	11.383	11.231	-36.36	1.261	17.921	1.19	16.787
BF	0.753													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S50: Bantu : Crow <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-56.96	19.022	1.881	4.725	1.07	13.671	10.166	16.189	5.362	-55.84	1.283	18.04	18.558	4.924
2	-57.01	18.995	1.907	4.755	1.065	13.61	10.374	16.133	5.571	-55.88	1.26	17.698	18.951	4.893
3	-56.89	19.072	1.916	4.736	1.058	13.501	10.363	16.241	5.434	-55.97	1.275	18.058	18.664	4.879
Mean	-56.95	19.03	1.901	4.739	1.064	13.594	10.301	16.188	5.456	-55.9	1.273	17.932	18.724	4.899
BF	-2.231													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S51: Bantu : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-58.393	14.028	3.116	2.389	1.2	6.522	9.485	5.252	4.025	-57.357	1.021	2.536	12.158	2.326
2	-58.324	14.076	3.103	2.382	1.212	6.787	9.544	5.329	4.035	-57.332	1.007	2.43	12.03	2.333
3	-58.377	13.979	3.153	2.362	1.191	6.621	9.334	5.212	4.096	-57.241	1.018	2.582	11.983	2.364
Mean	-58.365	14.028	3.124	2.378	1.201	6.643	9.454	5.264	4.052	-57.31	1.015	2.516	12.057	2.341
BF	-2.07													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S52: Bantu : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-56.612	2.768	1.112	14.599	1.733	2.826	1.422	10.263	14.536	-55.227	1.006	2.518	2.53	15.173
2	-56.706	2.791	1.087	14.687	1.776	2.711	1.445	10.097	14.638	-55.367	1.015	2.448	2.519	15.194
3	-56.672	2.809	1.094	14.769	1.773	2.802	1.439	10.178	14.584	-55.352	1.007	2.43	2.511	15.11
Mean	-56.663	2.789	1.098	14.685	1.761	2.78	1.435	10.179	14.586	-55.315	1.009	2.465	2.52	15.159
BF	-2.77													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S53: Bantu : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-60.055	3.092	1.279	18.826	3.927	7.162	4.153	8.473	11.61	-59.335	1.391	6.346	3.362	18.639
2	-60.145	3.111	1.267	18.837	3.904	7.084	4.184	8.717	11.652	-59.389	1.377	6.284	3.402	18.483
3	-59.917	3.097	1.263	18.648	3.827	7.109	4.065	8.385	11.312	-59.293	1.376	6.261	3.316	18.364
Mean	-60.039	3.1	1.27	18.77	3.886	7.118	4.134	8.525	11.525	-59.339	1.381	6.297	3.36	18.495
BF	-1.44													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S54: Bantu : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-71.5	6.828	1.406	20.283	2.408	7.765	5.858	7.939	9.5	-70.622	1.388	6.392	7.039	19.43
2	-71.426	6.783	1.456	20.199	2.395	8.138	5.929	7.728	9.358	-70.605	1.365	6.244	7.034	19.285
3	-71.384	6.853	1.426	20.222	2.376	7.822	5.895	7.779	9.483	-70.642	1.369	6.021	7.05	19.347
Mean	-71.437	6.821	1.429	20.235	2.393	7.908	5.894	7.815	9.447	-70.623	1.374	6.219	7.041	19.354
BF	-1.756													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S55: Bantu : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-68.9	2.27	1.632	4.953	1.811	7.149	2.989	11.692	12.583	-67.852	1.386	6.373	2.181	5.407
2	-69.01	2.262	1.661	4.806	1.82	7.435	2.975	11.673	12.592	-67.97	1.397	6.322	2.182	5.301
3	-68.922	2.273	1.681	4.824	1.809	7.429	2.936	11.755	12.461	-67.922	1.373	6.139	2.194	5.452
Mean	-68.944	2.268	1.658	4.861	1.813	7.338	2.967	11.707	12.545	-67.915	1.385	6.278	2.186	5.387
BF	-2.097													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S56: Bantu : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-73.417	1.107	2.71	14.119	10.485	3.136	3.914	2.567	14.346	-73.483	2.288	2.572	2.714	14.219
2	-73.314	1.095	2.729	13.652	10.269	3.206	3.845	2.518	14.117	-73.595	2.314	2.593	2.696	14.281
3	-73.237	1.113	2.689	13.827	10.36	3.179	3.812	2.48	14.081	-73.513	2.375	2.604	2.704	14.424
Mean	-73.323	1.105	2.709	13.866	10.371	3.174	3.857	2.522	14.181	-73.53	2.326	2.59	2.705	14.308
BF	0.132													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.001
Independent	1.000	1.000

Table S57: Bantu : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-80.57	3.105	1.476	10.029	8.312	6.022	9.368	2.798	2.642	-87.31	2.275	2.585	5.947	3.964
2	-80.49	3.045	1.484	9.947	8.365	6.102	9.606	2.81	2.659	-87.39	2.308	2.597	6.08	3.981
3	-80.37	3.151	1.528	9.959	8.302	6.21	9.332	2.794	2.684	-87.29	2.335	2.59	6.12	4.002
Mean	-80.48	3.1	1.496	9.978	8.326	6.111	9.435	2.801	2.662	-87.33	2.306	2.591	6.049	3.982
BF	13.494													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S58: Bantu : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-70.066	3.594	2.12	16.39	7.682	2.787	2.428	4.407	13.797	-69.06	2.257	2.65	3.112	16.955
2	-70.024	3.645	2.124	16.476	7.545	2.803	2.456	4.317	13.538	-69.042	2.223	2.598	3.108	16.877
3	-70.061	3.636	2.106	16.683	7.722	2.771	2.395	4.41	13.785	-69.048	2.239	2.61	3.118	16.955
Mean	-70.05	3.625	2.117	16.516	7.65	2.787	2.426	4.378	13.707	-69.05	2.24	2.619	3.113	16.929
BF	-2.012													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S59: Bantu : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-87.245	1.606	2.689	11.907	11.656	3.573	6.588	2.854	8.986	-89.474	2.703	2.685	4.125	8.698
2	-87.1	1.623	2.646	12.153	11.579	3.542	6.479	2.877	8.966	-89.409	2.72	2.672	4.159	8.996
3	-87.178	1.621	2.619	11.977	11.772	3.553	6.522	2.868	8.984	-89.459	2.654	2.667	4.134	8.957
Mean	-87.174	1.617	2.651	12.012	11.669	3.556	6.53	2.866	8.979	-89.447	2.692	2.675	4.139	8.884
BF	4.458													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S60: Bantu : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-79.123	14.122	5.772	3.675	3.359	6.596	17.602	2.675	3.188	-78.33	2.712	2.702	17.789	3.581
2	-79.051	14.266	5.791	3.697	3.441	6.584	17.413	2.652	3.246	-78.218	2.685	2.678	17.753	3.561
3	-79.209	14.273	5.842	3.684	3.468	6.728	17.444	2.662	3.203	-78.202	2.676	2.669	17.646	3.539
Mean	-79.128	14.22	5.802	3.685	3.423	6.636	17.486	2.663	3.212	-78.25	2.691	2.683	17.729	3.56
BF	-1.586													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S61: Bantu : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-84.198	14.459	7.409	3.398	3.372	3.4	18.168	3.191	5.269	-82.955	2.689	2.672	18.782	4.922
2	-84.14	14.678	7.317	3.396	3.275	3.449	18.311	3.193	5.265	-82.853	2.67	2.674	18.834	5.005
3	-83.9	14.514	7.441	3.334	3.324	3.462	18.109	3.176	5.303	-82.932	2.635	2.638	18.933	4.963
Mean	-84.079	14.55	7.389	3.376	3.324	3.437	18.196	3.187	5.279	-82.913	2.665	2.661	18.85	4.963
BF	-2.486													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table S62: Bantu : Omaha <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-70.562	4.869	2.25	8.616	0.739	10.969	1.765	14.163	12.403	-70.678	1.627	11.749	4.135	8.9
2	-70.529	4.81	2.229	8.691	0.728	10.911	1.788	13.862	12.767	-70.725	1.633	11.804	4.079	8.662
3	-70.488	4.819	2.23	8.647	0.737	10.861	1.84	14.007	12.381	-70.834	1.631	11.71	4.096	8.824
Mean	-70.526	4.833	2.236	8.651	0.735	10.914	1.798	14.011	12.517	-70.746	1.63	11.754	4.103	8.795
BF	0.232													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S63: Bantu : Omaha <-> Patrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-72.936	3.622	0.717	5.773	3.123	14.209	10.119	10.375	2.417	-74.604	1.657	11.807	3.241	4.127
2	-72.797	3.602	0.727	5.734	3.163	13.75	10.183	10.545	2.411	-74.537	1.646	11.773	3.189	4.087
3	-72.935	3.602	0.72	5.709	3.126	13.724	10.447	10.376	2.363	-74.607	1.611	11.609	3.195	4.097
Mean	-72.889	3.609	0.721	5.739	3.137	13.894	10.25	10.432	2.397	-74.583	1.638	11.73	3.208	4.104
BF	3.336													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S64: Bantu : Omaha <-> Patrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-69.50	19.426	0.871	8.128	1.91	13.444	13.605	10.198	1.899	-69.16	1.632	11.707	19.964	7.246
2	-69.45	19.311	0.915	8.118	1.952	13.63	13.447	10.14	1.902	-69.13	1.631	11.667	19.949	7.178
3	-69.39	19.431	0.884	8.182	1.954	13.6	13.468	10.218	1.925	-69.10	1.625	11.573	20.107	7.234
Mean	-69.44	19.389	0.89	8.143	1.939	13.558	13.507	10.185	1.909	-69.13	1.629	11.649	20.007	7.219
BF	-0.655													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S65: Bantu : Omaha <-> Patrilocal.strict

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-70.708	2.91	0.426	4.629	3.429	14.016	11.818	11.12	1.737	-73.92	1.628	11.779	2.79	3.553
2	-70.764	2.906	0.426	4.645	3.423	13.832	11.776	11.117	1.64	-73.886	1.617	11.611	2.775	3.556
3	-70.881	2.896	0.424	4.63	3.458	14.38	11.936	11.011	1.721	-73.766	1.613	11.584	2.777	3.573
Mean	-70.784	2.904	0.425	4.635	3.437	14.076	11.843	11.083	1.699	-73.857	1.619	11.658	2.781	3.561
BF	6.424													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.003
Independent	1.001	1.002

Table S66: Bantu : Omaha <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-65.26	18.788	1.103	5.61	1.818	13.393	13.456	10.613	1.868	-64.22	1.645	11.737	18.731	4.939
2	-64.86	18.814	1.087	5.616	1.849	13.315	13.24	10.723	1.82	-64.12	1.631	11.785	18.709	4.901
3	-64.95	19.088	1.088	5.663	1.844	13.639	13.155	10.658	1.863	-64.21	1.612	11.534	18.569	4.92
Mean	-65.02	18.897	1.093	5.63	1.837	13.449	13.284	10.665	1.85	-64.19	1.629	11.685	18.67	4.92
BF	-2.09													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table S67: Uto : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-21.01	11.078	10.815	2.362	16.985	4.446	9.342	7.851	2.193	-20.45	17.299	7.256	11.377	2.118
2	-20.963	11.011	10.926	2.342	17.017	4.439	9.616	7.858	2.264	-20.38	17.245	7.185	10.951	2.073
3	-20.862	11.16	11.105	2.292	16.978	4.311	9.298	7.933	2.205	-20.45	17.128	7.254	11.176	2.082
Mean	-20.945	11.083	10.949	2.332	16.993	4.399	9.419	7.881	2.221	-20.43	17.224	7.232	11.168	2.091
BF	-1.114													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

Table S68: Uto : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-20.186	2.033	17.534	11.31	9.369	7.466	1.974	5.066	17.712	-19.37	17.279	7.291	1.785	18.447
2	-20.141	2.068	17.475	11.169	9.319	7.557	1.95	4.952	17.707	-19.33	17.13	7.251	1.757	18.322
3	-20.17	2.014	17.439	10.877	9.037	7.476	1.919	4.849	17.433	-19.29	17.197	7.234	1.804	18.584
Mean	-20.166	2.038	17.483	11.119	9.242	7.5	1.948	4.956	17.617	-19.33	17.202	7.259	1.782	18.451
BF	-1.632													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S69: Uto : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-22.543	2.046	9.268	14.8	9.154	4.942	1.262	7.598	12.369	-21.76	11.513	6.152	1.298	16.03
2	-22.443	2.077	9.259	14.794	9.165	4.871	1.297	7.56	12.528	-21.79	11.527	6.142	1.319	16.143
3	-22.478	2.051	9.438	14.672	9.181	5.037	1.266	7.285	12.177	-21.787	11.788	6.214	1.289	15.93
Mean	-22.488	2.058	9.322	14.755	9.167	4.95	1.275	7.481	12.358	-21.779	11.609	6.169	1.302	16.034
BF	-1.567													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S70: Uto : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-30.775	8.311	9.53	10.87	11.001	4.341	5.867	9.315	13.714	-30.63	12.774	7.016	7.521	14.356
2	-30.651	8.501	9.562	11.08	11.166	4.404	5.834	9.123	13.545	-30.64	12.927	7.046	7.587	14.498
3	-30.579	8.401	9.297	10.802	11.189	4.185	5.732	8.967	13.385	-30.67	12.829	7.013	7.597	14.707
Mean	-30.668	8.404	9.463	10.917	11.119	4.31	5.811	9.135	13.548	-30.65	12.843	7.025	7.568	14.52
BF	-0.298													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S71: Uto : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-26.28	1.668	11.853	13.363	10.441	7.761	5.103	3.591	16.547	-26.20	12.714	6.925	3.791	18.639
2	-26.36	1.651	11.773	13.286	10.512	7.803	5.12	3.708	16.532	-26.13	12.713	6.921	3.755	18.874
3	-26.44	1.744	11.523	13.638	10.217	7.639	4.985	3.719	16.345	-26.16	12.578	6.891	3.777	18.75
Mean	26.36	1.688	11.716	13.429	10.39	7.734	5.069	3.673	16.475	-26.16	12.668	6.912	3.774	18.754
BF	-0.171													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S72: Uto : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-19.063	1.874	6.128	18.046	4.835	19.191	2.455	9.444	10.638	-18.30	6.008	18.784	1.774	18.58
2	-19.181	1.803	6.142	17.771	4.938	19.232	2.38	9.378	10.8	-18.33	6.029	18.792	1.775	18.544
3	-19.079	1.844	6.049	17.919	4.941	18.973	2.421	9.401	10.485	-18.25	6.017	18.811	1.778	18.477
Mean	-19.108	1.84	6.106	17.912	4.905	19.132	2.419	9.408	10.641	-18.28	6.018	18.796	1.776	18.534
BF	-1.607													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S73: Uto : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-21.001	2.198	6.215	9.527	4.62	18.329	2.978	11.337	12.544	-20.41	6.098	18.901	2.313	12.189
2	-21.062	2.199	6.212	9.481	4.489	18.401	2.981	11.133	12.646	-20.48	6.016	18.785	2.346	12.303
3	-21.042	2.164	6.214	9.399	4.54	18.54	2.98	11.208	12.415	-20.44	6.038	18.734	2.332	11.955
Mean	-21.035	2.187	6.214	9.469	4.55	18.423	2.98	11.226	12.535	-20.44	6.051	18.807	2.33	12.149
BF	-1.189													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S74: Uto : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-19.857	1.932	5.193	18.951	5.548	16.727	2.342	8.695	10.838	-19.20	5.327	16.263	1.785	19.204
2	-19.857	1.97	5.198	19.098	5.449	16.791	2.344	8.594	11.127	-19.09	5.349	16.39	1.775	19.377
3	-19.869	1.956	5.278	19.102	5.306	16.811	2.363	8.67	11.019	-19.14	5.398	16.558	1.769	19.544
Mean	-19.861	1.953	5.223	19.05	5.434	16.776	2.35	8.653	10.995	-19.14	5.358	16.404	1.776	19.375
BF	-1.319													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S75: Uto : Iroquois <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-23.396	2.502	2.665	15.353	9.714	15.527	6.503	9.305	7.858	-24.323	4.802	17.655	3.476	14.837
2	-23.429	2.602	2.668	15.99	9.751	15.819	6.594	9.478	7.882	-24.25	4.813	17.715	3.491	14.798
3	-23.556	2.538	2.711	15.703	9.558	15.598	6.439	9.431	7.899	-24.22	4.716	17.393	3.481	14.692
Mean	-23.46	2.547	2.681	15.682	9.674	15.648	6.512	9.405	7.88	-24.264	4.777	17.588	3.483	14.776
BF	1.854													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table S76: Uto : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-23.74	3.709	5.2	15.888	3.246	16.871	2.763	11.271	11.102	-23.11	4.764	17.368	3.48	16.716
2	-23.90	3.71	5.098	15.869	3.21	16.964	2.726	11.176	11.169	-23.18	4.718	17.329	3.385	16.708
3	-23.77	3.705	5.025	16.002	3.288	16.726	2.778	11.181	11.147	-23.20	4.748	17.52	3.417	16.697
Mean	-23.80	3.708	5.108	15.92	3.248	16.854	2.756	11.209	11.139	-23.16	4.743	17.406	3.427	16.707
BF	-1.269													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Table S77: Uto : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-21.56	2.016	1.526	13.847	12.606	15.418	14.468	7.107	4.671	-26.41	4.466	17.233	4.945	14.777
2	-21.74	1.999	1.571	13.764	12.671	15.368	14.612	7.226	4.677	-26.42	4.412	17.08	4.886	14.487
3	-21.82	2	1.549	13.637	13.198	15.486	14.877	7.239	4.588	-26.46	4.447	17.223	4.862	14.682
Mean	-21.71	2.005	1.549	13.749	12.825	15.424	14.652	7.191	4.645	-26.43	4.442	17.179	4.898	14.649
BF	9.705													

Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.000

Table S78: Uto : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	α1	β1	α2	β2
1	-25.58	5.895	1.555	19.537	10.054	16.03	13.63	9.314	4.858	-28.22	4.721	17.299	9.254	17.468
2	-25.69	5.995	1.607	19.745	9.926	16.301	13.722	9.422	4.883	-28.30	4.678	17.135	9.263	17.446
3	-25.61	6.066	1.56	20.025	9.889	16.235	13.52	9.286	4.752	-28.26	4.812	17.359	9.356	17.475
Mean	-25.63	5.985	1.574	19.769	9.956	16.189	13.624	9.341	4.831	-28.26	4.737	17.264	9.291	17.463
BF	5.29													

Gelman-Rubin MCMC chain diagnostic test

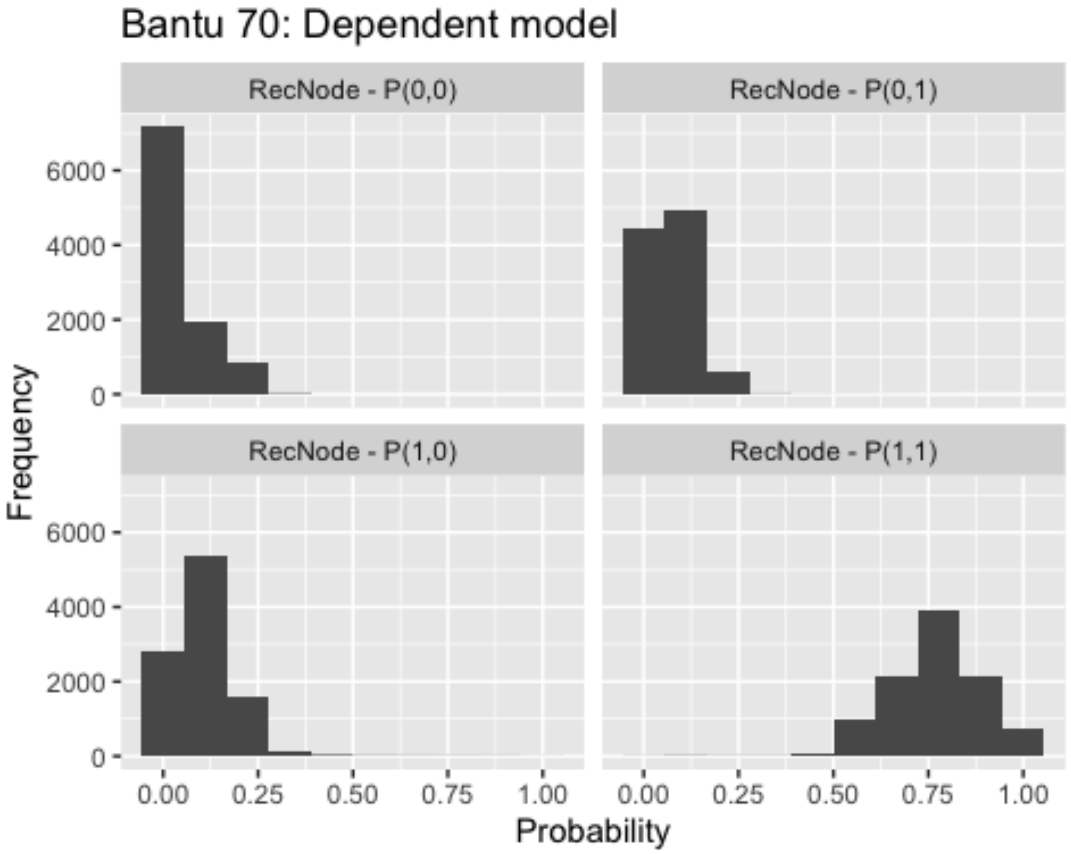
	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Bantu node 70 state inference

Here we re-construct node 70 within the Bantu tree, to confirm the hypotheses that the presence of both Iroquois terminologies and a preference for cross-cousin marriage existed at this point.

Table 1 in the main text shows that the dependent model is already preferred, so here we only look at the dependent model. The figure below shows the likelihood of each possibility. Top left: Absence of both Iroquois terminology and a preference for cross-cousin marriage. Top right: Absence of cross-cousin marriage and the presence of cross-cousin marriage preference. Bottom right: Both Iroquoian terminologies and cross-cousin marriage preferences are present. Bottom left: presence of an Iroquoian terminology, and absence of a cross-cousin marriage preference.

The graph clearly shows the presence of both traits being present here is the most likely option, with approximately 0.77 probability. This probability drops to around 0.5 on the ancestral node.



Multiple comparisons

Since this study has numerous hypothesis tests, it is important we address the statistical problem of multiple comparisons. The multiple comparison problem says that the more hypotheses tested simultaneously, the more likely an erroneous error is to occur. There is strong debate in the literature on whether this is a problem here, but we argue that it is not.

The primary reason for this not being a problem is that all our hypotheses were set out *a priori*. They are not the result of comparing all social variables against all binary kinship terminologies and make up a tiny portion of those that are possible. All hypotheses are established in theory and many had been previously tested.

Phylogenetic Inertia

We were concerned that a prevalence of phylogenetic inertia was the primary reason for not finding many significant co-evolutionary relationships. That is, kinship terminologies and social organisation are so tightly tied, that we would not be able to detect a relationship using this approach. To assess how prevalent this was in our results we reviewed each hypothesis on 3 criteria; 1) What was the most likely independent ancestral state, 2) How likely was that ancestral state, and 3) How are the two variables distributed across the respective phylogenies. In an independent model (where each trait changes independent of the other) we would expect that if the ancestral state shows the presence of both traits, there is a possibility that both traits were inherited over time, either by chance or due to a stable relationship. In both these cases, our phylogenetic approach would fail to pick up a relationship between these traits. The second criteria give us a level of confidence in the first criteria, we assume a probability of above 0.7 indicates a high likelihood of the true ancestral state. The third criteria allow us to qualitatively review whether we think the methods are failing to detect a relationship, by visualizing the data on mirrored phylogenies. The first two criteria mean that it is plausible that two traits are ancestral, but unrelated, by looking at the distribution of traits on a tree, we can assess whether this is the case or not. Visualization also allows us to attest whether stable pairings occur later within a lineage. These plots can be found in the figures folder in the GitHub repository. Using the three criteria above, we then decide if a hypothesis is likely to be influenced by phylogenetic inertia on a four-point scale, ranging from highly likely to highly unlikely. The table below shows these judgments, and ancestral state criteria, for all hypotheses that we did not find support for. These decisions were independently decided on by each author and then conferred on the result.

Table S85: Judgments of phylogenetic inertia. The first columns show our overall judgements. The second column shows the most likely ancestral state in an independent model of evolution, organised as [Kin terminology], [social structure]. The third column shows the probability of this state.

hypothesis	Most likely ancestral state	Probability of ancestral state	judgement
austronesian-crow-high.polygyny	0,0	0.99	Highly unlikely
austronesian-crow-polygyny	0,1	0.64	Unlikely
austronesian-eskimo-absenceofcousinmarriage.permitted	1,1	0.42	Unlikely
austronesian-eskimo-absenceofcousinmarriage.preference	1,0	0.81	Highly unlikely
austronesian-eskimo-bi.linealdescent	1,0	0.91	Highly unlikely
austronesian-eskimo-neo.localresidence	1,0	0.79	Highly unlikely
austronesian-eskimo-nuclear.families	1,1	0.74	**Likely**
austronesian-hawaiian-absenceofcousinmarriage.permitted	1,1	0.43	Unlikely
austronesian-hawaiian-absenceofcousinmarriage.preference	1,0	0.52	Unlikely
austronesian-hawaiian-bi.linealdescent	0,0	0.44	Unlikely
austronesian-hawaiian-bi.localextendedfamily	1,1	0.3	Unlikely
austronesian-hawaiian-bi.localresidence	1,0	0.5	Highly unlikely
austronesian-iroquois-exogamy.unilineal.descent	0,0	0.99	Highly unlikely
austronesian-iroquois-high.polygyny	0,0	0.99	Highly unlikely
austronesian-iroquois-matri.anvunclocalresidence	0,0	0.96	Highly unlikely
austronesian-iroquois-polygyny	0,1	0.62	Highly unlikely
austronesian-iroquois-uni.linealdescent	0,0	0.92	Highly unlikely
bantu-crow-matri.anvunclocalresidence	0,0	0.65	Highly unlikely
bantu-crow-matrilineal	0,0	0.68	Highly unlikely
bantu-crow-matrilocal	0,0	0.97	Highly unlikely
bantu-crow-uni.localresidence	0,1	0.95	Highly unlikely
bantu-hawaiian-absenceofcousinmarriage.permitted	0,1	0.879	Highly unlikely
bantu-hawaiian-absenceofcousinmarriage.preference	0,0	0.9	Highly unlikely
bantu-hawaiian-bi.linealdescent	0,0	0.89	Highly unlikely
bantu-hawaiian-bi.localextendedfamily	0,0	0.73	Highly unlikely
bantu-hawaiian-bi.localresidence	0,0	0.92	Highly unlikely
bantu-iroquois-cross.cousinmarriage.preferred	1,1	0.51	Highly likely
bantu-iroquois-exogamy.unilineal.descent	0,0	0.44	Highly unlikely
bantu-iroquois-uni.linealdescent	1,1	0.59	Unlikely
bantu-iroquois-uni.localresidence	1,1	0.5	**Likely**
bantu-omaha-uni.localresidence	0,1	0.93	Highly unlikely
uto-hawaiian-absenceofcousinmarriage.permitted	1,1	0.98	Unlikely
uto-hawaiian-absenceofcousinmarriage.preference	1,0	0.99	**Likely**
uto-hawaiian-bi.linealdescent	1,0	0.98	Highly unlikely
uto-hawaiian-bi.localextendedfamily	1,0	0.74	Unlikely

uto-hawaiian-bi.localresidence	1,0	0.98	Unlikely
uto-iroquois-cross.cousinmarriage.permitted	0,0	0.99	Highly unlikely
uto-iroquois-cross.cousinmarriage.preferred	0,0	0.99	Highly unlikely
uto-iroquois-exogamy.unilineal.descent	0,0	0.99	Highly unlikely
uto-iroquois-high.polygyny	0,0	0.99	Highly unlikely
uto-iroquois-matri.anvunclocalresidence	0,0	0.95	Highly unlikely
uto-iroquois-uni.linealdescent	0,0	0.99	Highly unlikely
uto-iroquois-uni.localresidence	0,0	0.49	Highly unlikely

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Chapter 3 App

APPENDIX B

Appendix B: Supplementary Material for Chapter 3

Kinbank: Database

Supplementary Material

Kinbank on github

All data for Kinbank is held within the github repository:
https://github.com/kinbank/kinbank

In the github repository the location of the cldf format data is in kinbank/cldf/

This folder contains the following six files, which are described in table S1. For detailed information see: https://github.com/cldf/cldf

Table S3.1: CLDF table descriptions of Kinbank.

File	Description
cldf-metadata.json	This is a metadata description file, which contains a json description of each file in the cldf folder, and each column within those files to ensure the data is formatted correctly.
forms.csv	This contains the forms, or kinterms, for each language. This file links to the languages file by the Languages_ID column, parameters file by the Parameters_ID column, and the sources file by the sources_bibtex column.
languages.csv	This file contains metadata on each language (glottocode, geographic coordinates etc.)
parameters.csv	This file contains descriptions of each kin-type used in the dataset.
Sources.bib	A bibtex file containing information on the sources used in Kinbank.
requirements.txt	This file contains the python package requirements for installing Kinbank

Table S 1: Description of CLDF tables in Kinbank

Core kin types

Table S3.2: Core kin types used for primary search criteria in Kinbank. If concepts were available, but not in this set, they were added to the database, but were not the focus of collection. See https://github.com/cldf/cldf for the full list of concepts.

Siblings, Parents, Parent's siblings, Grandparents		Cousins		Affines	
Parameter	***Description***	***Parameter***	***Description***	***Parameter***	***Description***
G	sibling	FeBS	father's older brother's son	E	spouse
eB	elder brother	FyBS	father's younger brother's son	H	husband
yB	younger brother	FeZS	father's older sister's son	W	wife
eZ	elder sister	FyZS	father's younger sister's son	HF	husband's father
yZ	younger sister	FeBD	father's older brother's daughter	HM	husband's mother
P	parent	FyBD	father's younger brother's daughter	WF	wife's father
F	father	FeZD	father's older sister's daughter	WM	wife's mother
M	mother	FyZD	father's younger sister's daughter	BW	brother's wife
C	child	MeBS	mother's older brother's son	ZH	sister's husband
S	son	MyBS	mother's younger brother's son	WB	wife's brother
D	daughter	MeZS	mother's older sister's son	WZ	wife's sister
A	ancestor	MyZS	mother's younger sister's son	HB	husband's brother
PP	grandparent	MeBD	mother's older brother's daughter	HZ	husband's sister
FF	father's father	MyBD	mother's younger brother's daughter	co-W	co-wife
FM	father's mother	MeZD	mother's older sister's daughter	co-H	co-husband
MF	mother's father	MyZD	mother's younger sister's daughter	FW(notM)	father's wife (not mother)
MM	mother's mother	FBeS	father's brother's older son	MH(notF)	mother's husband (not father)
CC	grandchild	FByS	father's brother's younger son	SW	son's wife
SS	son's son	FZeS	father's sister's older son	SWM	son's wife's mother
SD	son's daughter	FZyS	father's sister's younger son	SWF	son's wife's father
DS	daughter's son	FBeD	father's brother's older daughter	DH	daughter's husband
DD	daughter's daughter	FByD	father's brother's younger daughter	DHM	daughter's husband's mother
FeB	father's older brother	FZeD	father's sister's older daughter	DHF	daughter's husband's father
FyB	father's younger brother	FZyD	father's sister's younger daughter	FZH	father's sister's husband
FeZ	father's older sister	MBeS	mother's brother's older son	FBW	father's brother's wife
FyZ	father's younger sister	MByS	mother's brother's younger son	MZH	mother's sister's husband
MeZ	mother's older sister	MZeS	mother's sister's older son	MBW	mother's brother's wife
MyZ	mother's younger sister	MZyS	mother's sister's younger son		
MeB	mother's older brother	MBeD	mother's brother's older daughter		
MyB	mother's younger brother	MByD	mother's brother's younger daughter		
eBS	older brother's son	MZeD	mother's sister's older daughter		
yBS	younger brother's son	MZyD	mother's sister's younger daughter		
eBD	older brother's daughter				
yBD	younger brother's daughter				
eZS	older sister's son				
yZS	younger sister's son				
eZD	older sister's daughter				
yZD	younger sister's daughter				

Are you my *mama*?

Model summary

Table S3.3: Table of coefficients for the phylogenetically-controlled repeated measures multi-level Bayesian logistic regression. Significant coefficients are in bold.

Family: bernoulli
  Links: mu = logit
Formula: mother ~ vowel + consonant + (1 | gr(super_tree, cov = A)) + (1 | Glottocode)
   Data: df (Number of observations: 3068)
Samples: 4 chains, each with iter = 5000; warmup = 2000; thin = 1;
         total post-warmup samples = 12000

Group-Level Effects:
~Glottocode (Number of levels: 991)
              Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)   0.05   0.04   0.00   0.15 1.00   5569   4870

~super_tree (Number of levels: 991)
              Estimate   Est.Error   l-95% CI u-95% CI Rhat Bulk_ESS Tail_ESS
sd(Intercept)   0.00   0.00   0.00   0.00 1.00   3884   5388

	Estimate	*Est.Error*	*lower 95% CI*	*Upper 95% CI*	*Rhat*	*Bulk_ESS*	*Tail_ESS*
Intercept	0.32	0.92	-1.46	2.17	1	2049	3434
vowel3	-0.35	1.1	-2.53	1.78	1	3124	5134
vowela	-0.42	0.86	-2.15	1.24	1	2207	3287
vowele	0.43	0.87	-1.31	2.13	1	2263	3515
vowelE	1.01	1.01	-1	2.98	1	2718	4667
voweli	1.12	0.86	-0.61	2.79	1	2233	3506
vowelo	-0.8	0.88	-2.57	0.88	1	2266	3418
vowelu	-0.07	0.87	-1.81	1.63	1	2248	3459
consonant5	0.07	1.77	-3.57	3.64	1	12165	7997
consonant7	-0.32	0.61	-1.54	0.86	1	4112	6629
consonant8	-1.89	1.39	-5.06	0.44	1	7657	6294
consonantb	**-1.64**	**0.36**	**-2.35**	**-0.94**	**1**	**1706**	**3662**
consonantc	-1.28	0.8	-2.87	0.27	1	5953	7578
consonantC	-1.01	0.54	-2.09	0.01	1	3326	5652
consonantd	-0.44	0.39	-1.21	0.32	1	2017	4102
consonantf	**-1.31**	**0.51**	**-2.31**	**-0.33**	**1**	**3150**	**6267**
consonantg	0.13	0.46	-0.8	1.03	1	2593	5222
consonantG	2.2	1.38	-0.1	5.38	1	9746	7001
consonanth	-0.52	0.43	-1.36	0.33	1	2380	4925
consonantj	0.3	0.48	-0.63	1.26	1	2850	5042
consonantk	0.13	0.36	-0.58	0.83	1	1654	3513
consonantl	-0.2	0.46	-1.11	0.68	1	2655	5284
consonantm	0.09	0.32	-0.53	0.72	1	1430	2658
consonantn	**1.03**	**0.34**	**0.37**	**1.7**	**1**	**1578**	**3270**
consonantN	**1.44**	**0.37**	**0.71**	**2.16**	**1**	**1728**	**3659**
consonantp	**-2.02**	**0.36**	**-2.73**	**-1.34**	**1**	**1702**	**3661**
consonantr	**-0.91**	**0.45**	**-1.79**	**-0.02**	**1**	**2615**	**4956**
consonants	**-1.1**	**0.38**	**-1.85**	**-0.37**	**1**	**1868**	**4011**
consonantS	-0.77	0.97	-2.68	1.16	1	8193	8284
consonantt	**-1.69**	**0.34**	**-2.34**	**-1.03**	**1**	**1565**	**3008**
consonantv	0.03	0.52	-0.97	1.07	1	3204	6087
consonantw	0.57	0.41	-0.24	1.36	1	2176	4513
consonantx	-8.22	6	-22.63	0.43	1	10224	6969
consonantX	0.83	1.02	-1.06	2.95	1	7476	7187
consonanty	-0.11	0.36	-0.83	0.6	1	1708	3520
consonantz	-1.58	1.04	-3.75	0.38	1	9006	7707

It’s ok we’re not cousins by culture.

Cross-cousin marriage coding

This section contains the coding scheme used to binarize *EA023: Cousin marriages permitted* variable taken from the Ethnographic Atlas dataset on D-PLACE.

Table S3.4: Coding decisions for EA023 from the ethnographic atlas used to derive a binary cross-cousin marriage variable.

Type of marriage	**Coding**
Duolateral cross-cousin marriage permitted, i.e., marriage allowed with either MoBrDa or FaSiDa but forbidden with a parallel cousin	1
Duolateral marriage permitted with paternal cousins only (FaBrDa or FaSiDa)	1
Duolateral marriage permitted with maternal cousins only (MoBrDa or MoSiDa)	1
Duolateral marriage permitted with an uncle's daughter only (FaBrDa or MoBrDa)	1
Duolateral marriage permitted with an aunt's daughter only (FaSiDa or MoSiDa)	1
Unilateral: only matrilateral cross-cousin marriage permitted, i.e., with a MoBrDa	1
Nonlateral marriage, i.e., unions forbidden with any first or second cousin	0
Nonlateral marriage, evidence available only for first cousins	0
Unilateral: only patrilateral cross-cousin marriage permitted i.e., with a FaSiDa	1
Quadrilateral marriage, i.e., marriage allowed with any first cousin	0
Nonlateral marriage in which all first cousins and some but not all second cousins are forbidden as spouses	1
Nonlateral marriage in which unions are forbidden with any first cousin but are permitted with any second cousin (or at least any who is not a lineage mate)	0
Trilateral marriage, i.e., marriage allowed with any first cousin except an orthocousin or lineage mate	0

Bifurcate merging data

This table contains data on the presence/absence of bifurcate merging in each language used in the analysis, their taxon code used in the Grollemund et. al (2015) phylogeny.

Table S3.5: Bifurcate merging codes, derived from Kinbank, for 61 Bantu languages, alongside their taxa codes used in the Grollemund et al. (2015) phylogeny.

Name	Taxon	Male BM	Female BM	Complete BM
Bakweri	A22_Bakweri	1	0	0
Batanga	A32C_Batanga	1	1	1
Fang Bitam	A75a_Fang_Bitam	1	1	1
Kota	B25_Kota	1	1	1
Mbunda	B84_Mbunda	1	1	1
Yanzi	B85_Yanzi	0	0	0
Nsongo	B85d_Nsongo	1	1	1
Dinga	B86_Dinga	1	1	1
Bushong	C61E_Konda	1	1	1
Songola	C71_Tetela	1	1	1
Kikuyu	C83_Bushong	1	1	1
Meru	D24_Songola	1	0	0
Digo	E51_Kikuyu	1	0	0
Bende	E53_Meru	1	1	1
Giryama	E72a_Giryama	1	1	1
Digo	E73_Digo	1	1	1
Bende	F12_Bende	1	1	1
Sukuma	F21_Sukuma	1	1	1
Fefe Grassfields	Fefe_Grassfields	0	0	0
Gogo	G11_Gogo	1	1	1
Kagulu	G12_Kagulu	0	0	0
Kwere	G32_Kwere	1	1	1
Nguungulu	G34_Nguungulu	-1	1	0
Luguru	G35_Luguru	1	1	1
Sangu	G61_Sangu	1	1	1
Hehe	G62_Hehe	1	1	1
Bena	G63_Bena	1	1	1
Kisikongo (2013)	H16a_Kisikongo_2013	1	-1	0
Yombe	H16c_Yombe	1	1	1
Suku	H32_Suku	1	1	1
Mbala	H41_Mbala	1	1	1
Shi	JD53_Shi	1	1	1
Rundi	JD62_Rundi	0	0	0
Kiha	JD66_Kiha	1	1	1
Runyoro	JE11_Runyoro	1	1	1
Luganda	JE15_Luganda	1	1	1
Lusoga	JE16_Lusoga	0	1	0
Haya	JE22_Haya	0	1	0
Kerebe	JE24_Kerebe	1	1	1
Bukusu	JE31c_Bukusu	1	1	1
Gusii	JE42_Gusii	1	-1	0
Ciokwe	K11_Ciokwe	1	1	1
Lwena	K14_Lwena	1	1	1
Lozi	K21_Lozi	0	0	0
Pende	L11_Pende	1	1	1
Luba-Kasai	L31a_Luba-Kasai	1	1	1
Sanga	L35_Sanga	1	-1	0
Kaonde	L41_Kaonde	1	1	1
Lunda	L52_Lunda	1	1	1
Fipa	M13_Fipa	1	1	1
Bemba	M42_Bemba	1	1	1
Lamba	M54_Lamba	1	1	1
Tonga	M64_Tonga	1	0	0
Ngoni	N12_Ngoni	1	1	1
Simakonde	P23_Simakonde	1	1	1
Umbundu	R11_Umbundu	1	1	1
Herero	R31_Herero	0	1	0
Venda	S21_Venda	1	1	1
Tswana	S31_Tswana	1	1	1
Zulu	S42_Zulu	1	1	1
Tsonga	S53_Tsonga	1	1	1

MCMC trace plots

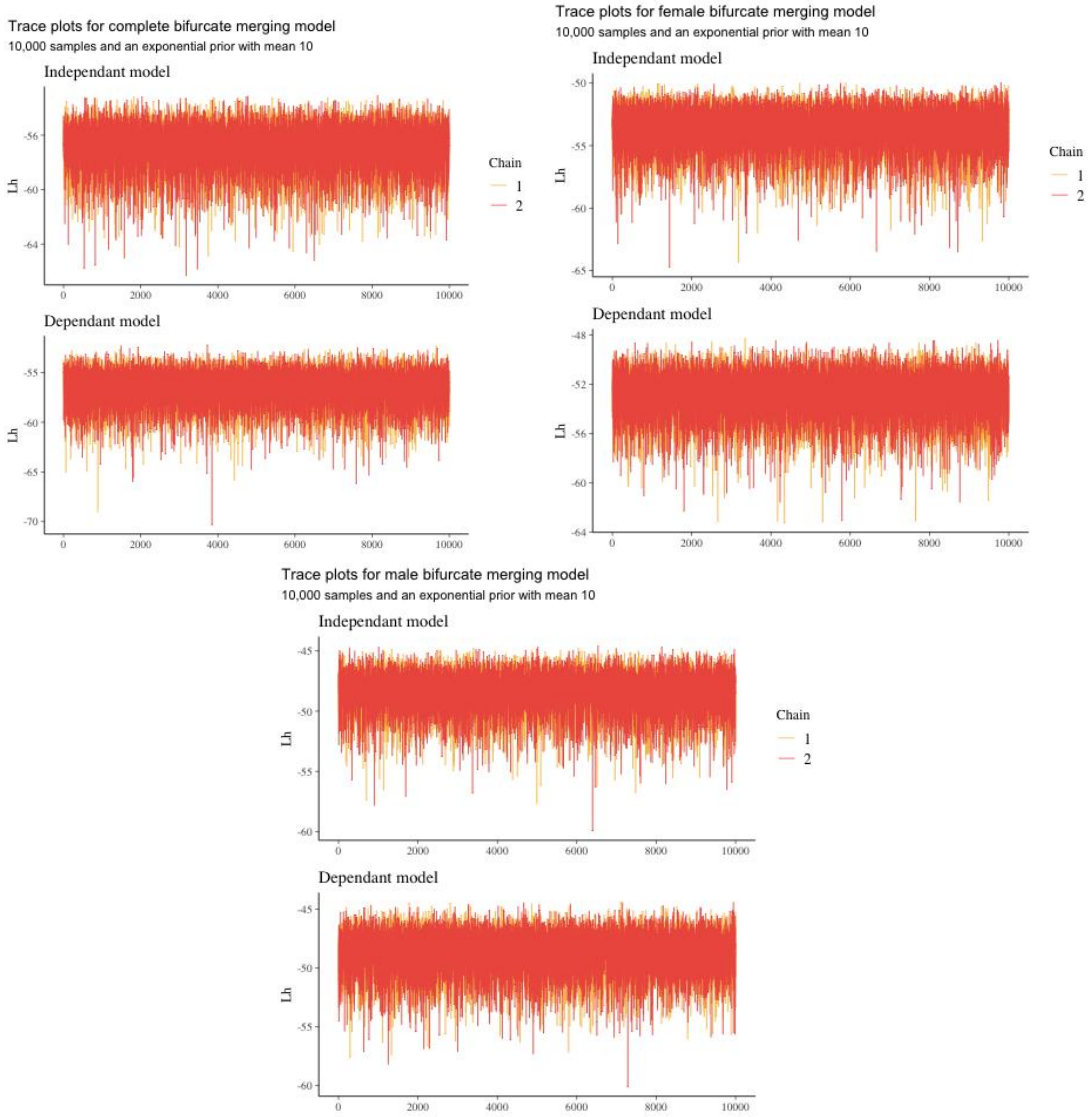


Figure S3.1: Model convergence plots for each of the three co-evolutionary models (male bifurcate merging, female bifurcate merging, and complete bifurcate merging). Each model is a sample of 10,000 iterations over two chains. All models are seen to converge.

Chapt 5 App

Appendix C: Supplementary Material for Chapter 5

HDBSCAN Settings

The HDBSCAN algorithm was implemented using the hdbscan python library (McInnes, Healy, and Astels 2017). Table S5.1 shows the settings used for each algorithm. Min Samples was chosen based on the value that minimised outliers.

Table S1: HDBSCAN settings for each subset of kin terms. Min samples was chosen based on the value that minimised outliers.

Subset	alpha	leaf size	metric	Min cluster size	min samples
Siblings	1	100	Jaccard	10	3
G^0	1	100	Jaccard	10	3
G^{+1}	1	100	Jaccard	10	3
G^{+2}	1	100	Jaccard	10	8
G^{-1}	1	100	Jaccard	10	3

Decision trees

To make the typological results of practical use, the HDBSCAN output is run through a decision tree algorithm to determine what features best describe each category.

The decision tree algorithm cannot perfectly determine the categorisation of each subset of kin terms, therefore each decision tree is affiliated with an accuracy score, where 1.0 is equivalent to 100% accuracy. Uncategorised languages are excluded from the decision tree analysis.

Each decision tree is pyramid of boxes and arrows. Each box contains the following information:

Feature: Within kinspace each feature is the comparison of two kin types. If both kin types have the same kin term, they are coded as 1, if they are different, they are coded as zero. If the equation in the decision tree is true, follow the arrows to the left, if the equation is false follow to the right. In the example we have the equation myZmeZ <= 0.5 – if a language has a single sister term for male speakers this statement would be false because myZ and meZ would be the same and therefore be coded as 1. If a language distinguishes relative age for sisters when a male is speaking then myZmeZ <= 0.5 would be true.

Entropy: This value indicates how much disorder there is in the remaining sample. In the first box entropy is high. In a terminal box with no misclassification, entropy is zero. Comparing entropy between connected boxes indicates how much information is gained from that link.

Samples: The number of languages uncategorized at this point in the decision tree.

Value: The number of languages from each category left uncategorised. Comparing samples and values in terminal nodes indicates how many languages were correctly categorised for any particular category.

Class: The most likely class of this box. Most useful in terminal boxes.

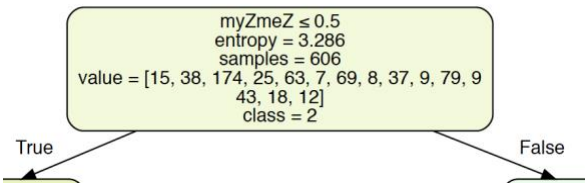


Figure S5.1: Decision tree for the sibling typology. The decision tree categorises languages with 98% accuracy

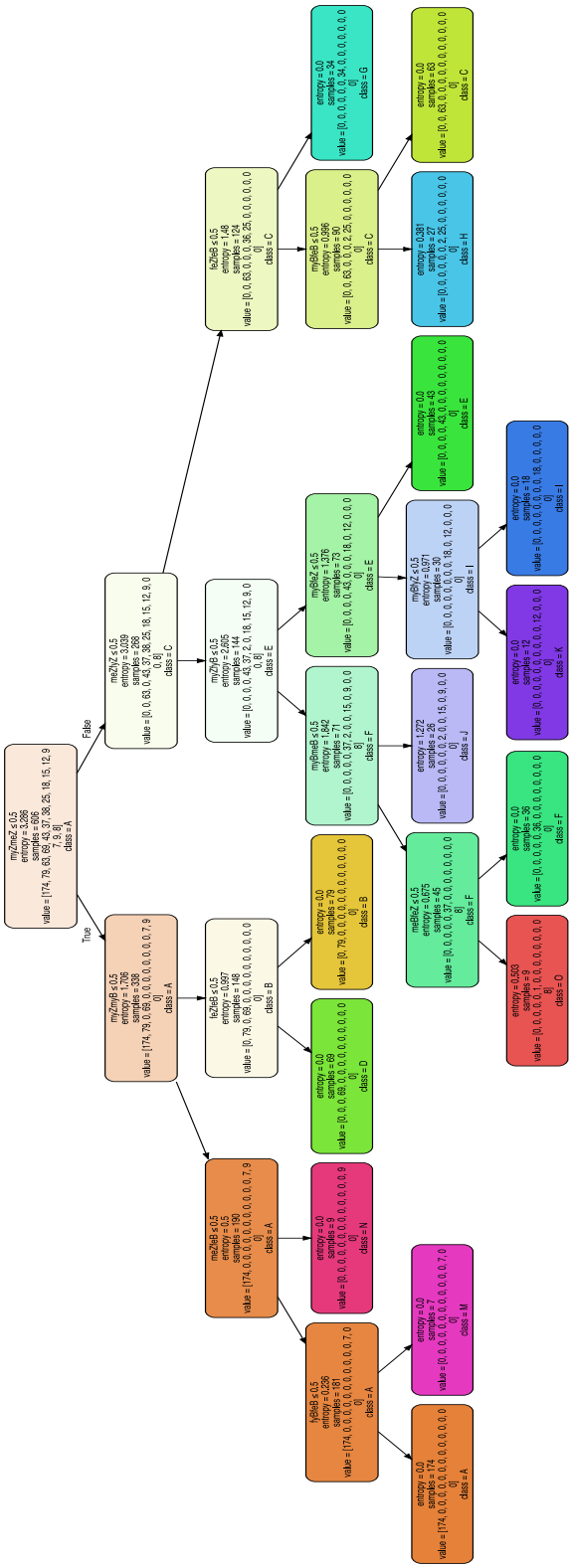


Figure S5.2: Decision tree for the G^0 typology. The decision tree categorises languages with 94% accuracy

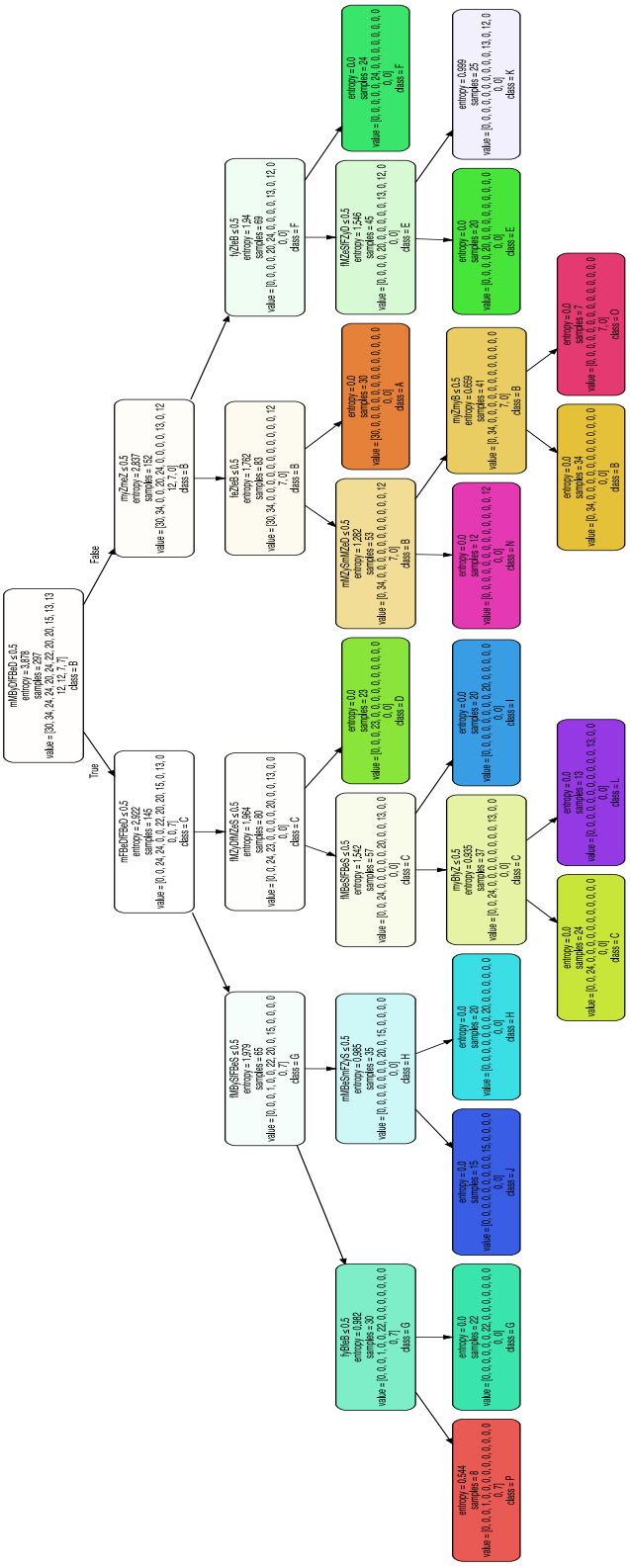


Figure S5.3: Decision tree for the G^{+1} typology. The decision tree categorises languages with 97% accuracy

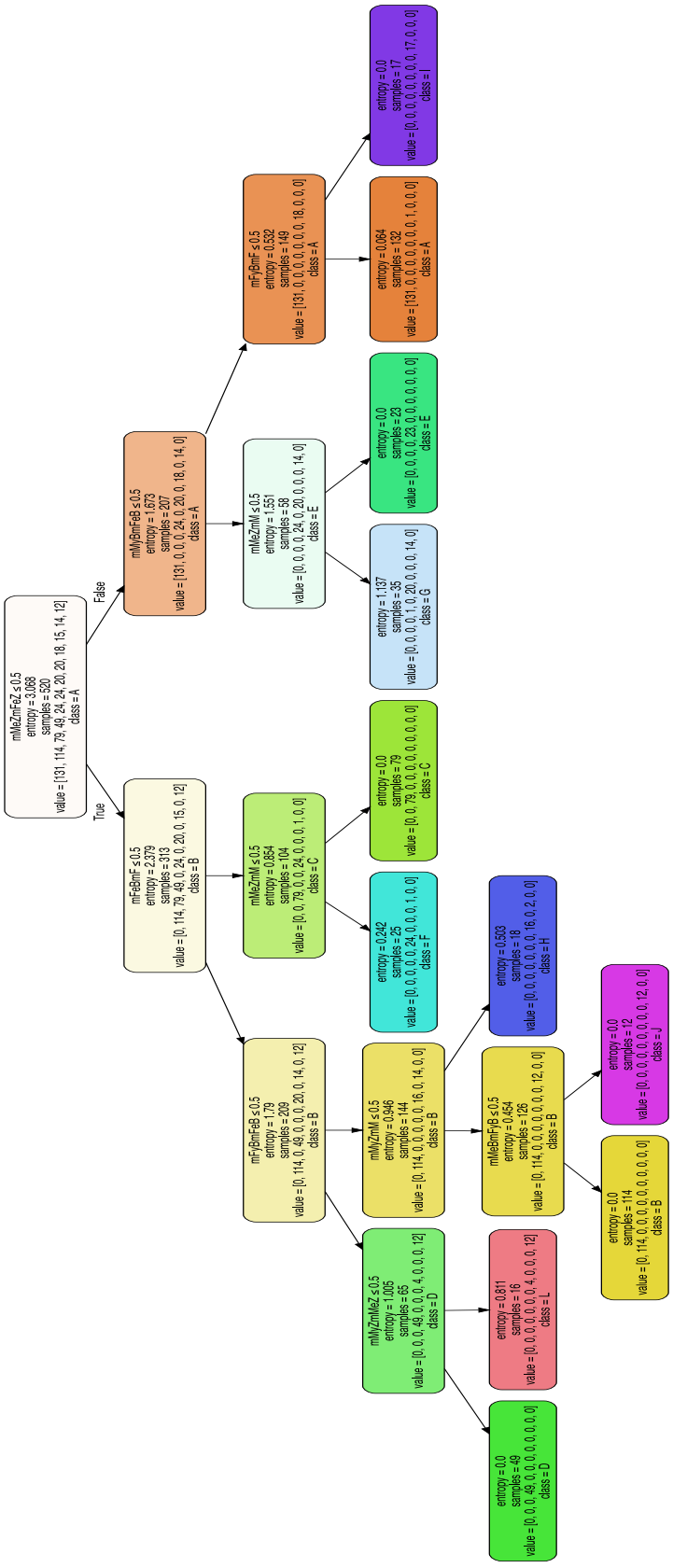


Figure S5.4: Decision tree for the G^{+2} typology. The decision tree categorises languages with 99% accuracy

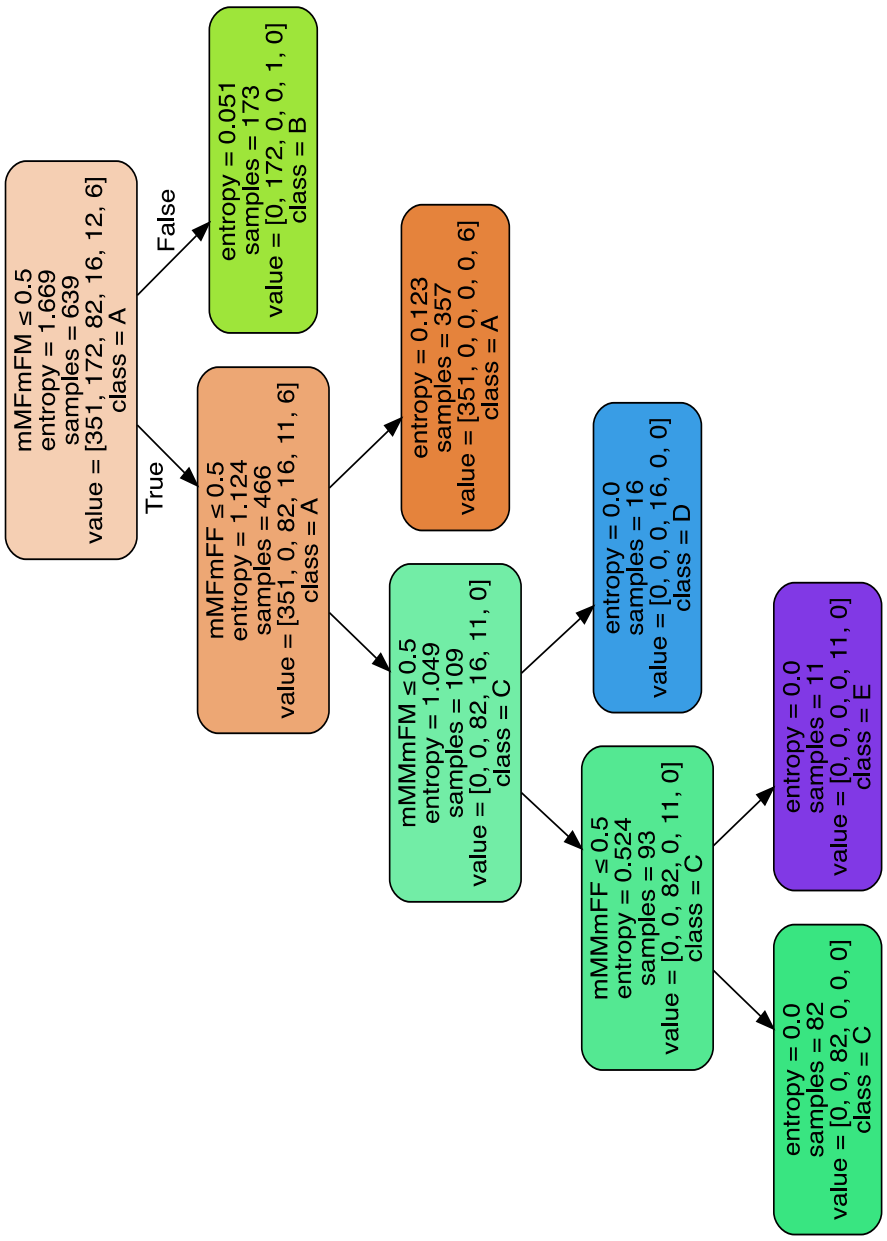
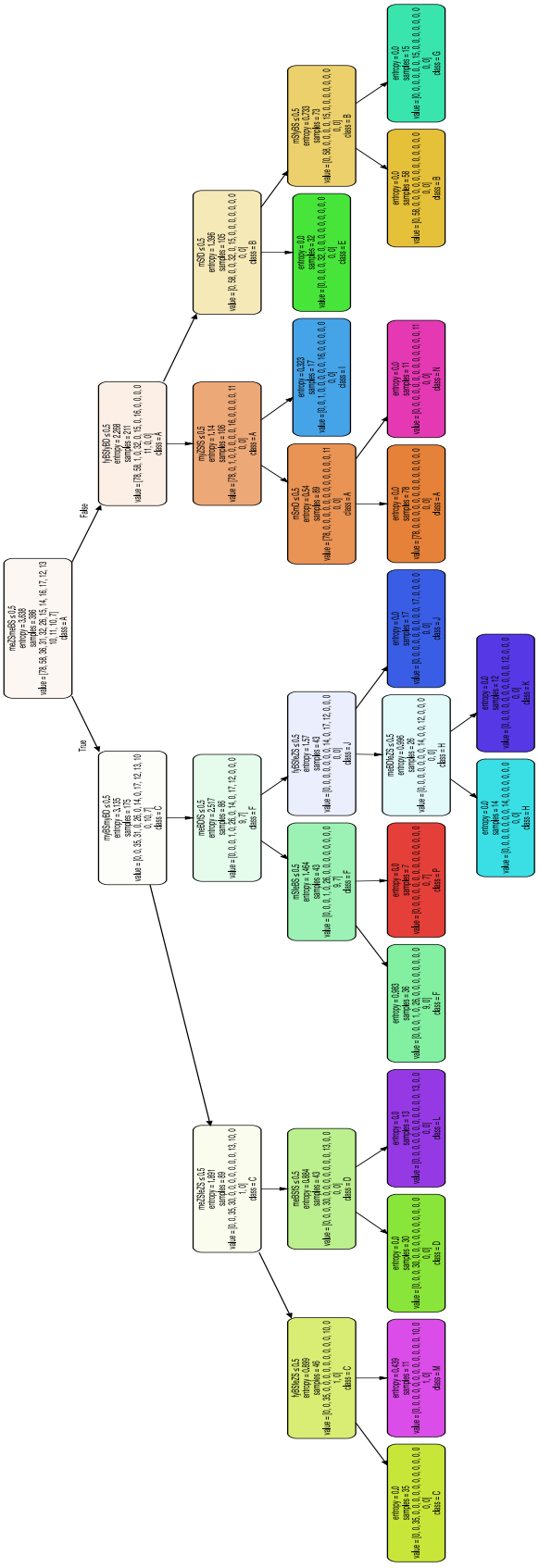


Figure S5.5: Decision tree for the G^0 typology. The decision tree categorises languages with 100% accuracy.



Networks

Figure 5.9 in the main text shows the network created for sibling typologies. Here we display the same figure for each of the remaining four kin type subsets. The following graphs are laid out the same way: nodes are type derived from kinspace, edges are rue changes to move between organisations.

In the graphs below, each node is labelled with the letter used in the main text tables descrying the categories (rather than the descriptive code used in figure 5.9). If nodes are labelled using a lowercase letter, these are unobserved types which were created to connect the graph. These are described within their respective sections in tables with the label and the coded description, as is used in the main text. -

Figure S5.6: Network for the G^0 typology. This network contains four unobserved types to ensure a connected network.

Unobserved types

label	Coded description
a	(B FBS MZS)(Z FBD FZD)(FZS FZD)(FZD MBD)
b	(B FBS MZS)(Z FBD FZD)(FZS FZD)(FZD MBD)
c	(B Z FBS FBD FZS FZD MBS MBD ZS MZD)
d	X // (FBS FBD MZS MZD)(FZS FZD MBS MBD)

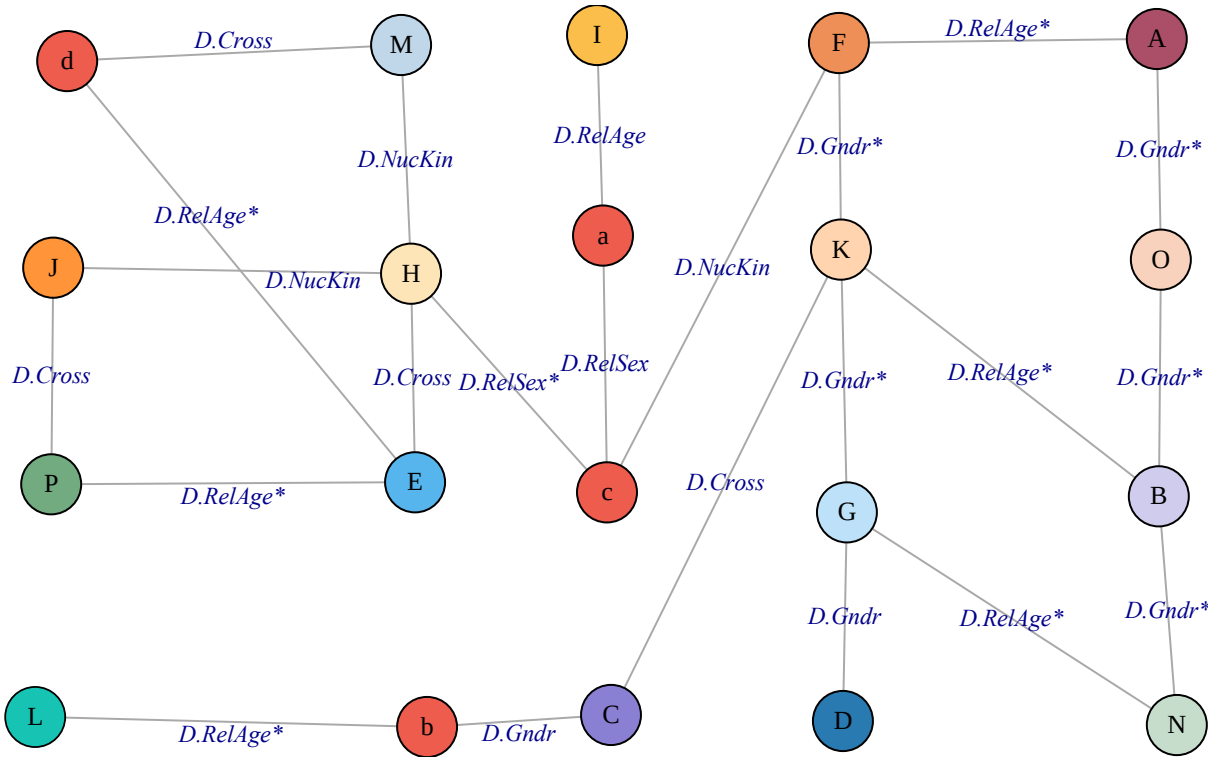


Figure S5.7: Network for the G^{+1} typology.

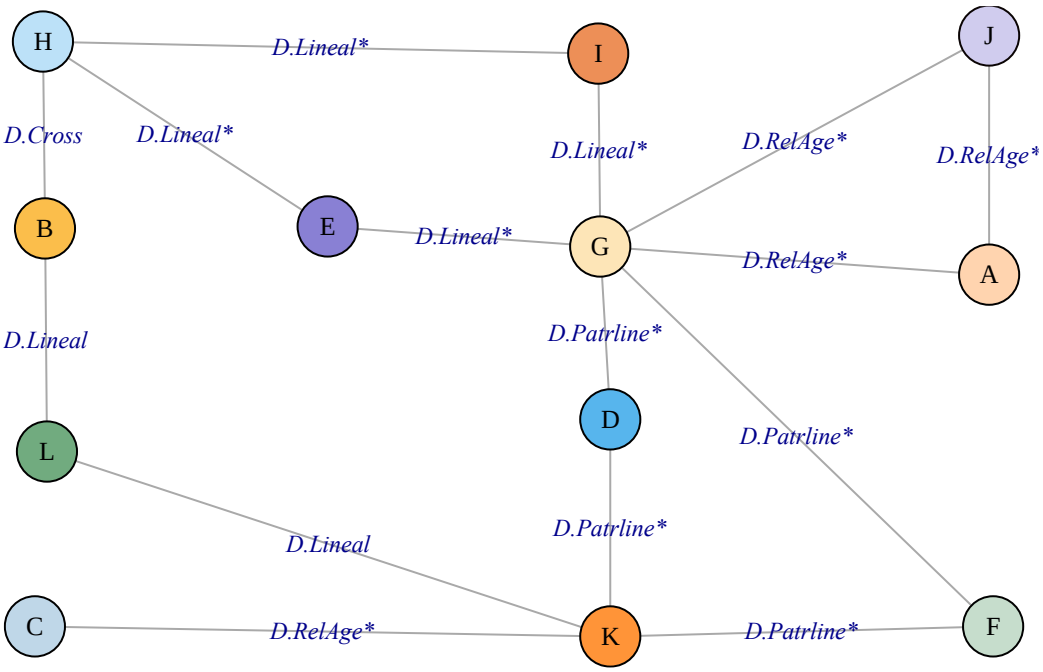


Figure S5.8: Network for the G^{+2} typology.

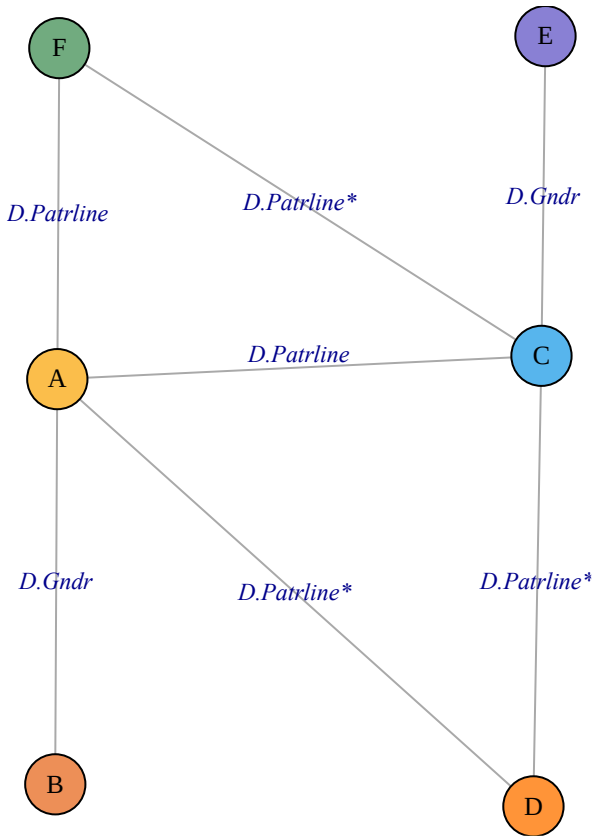
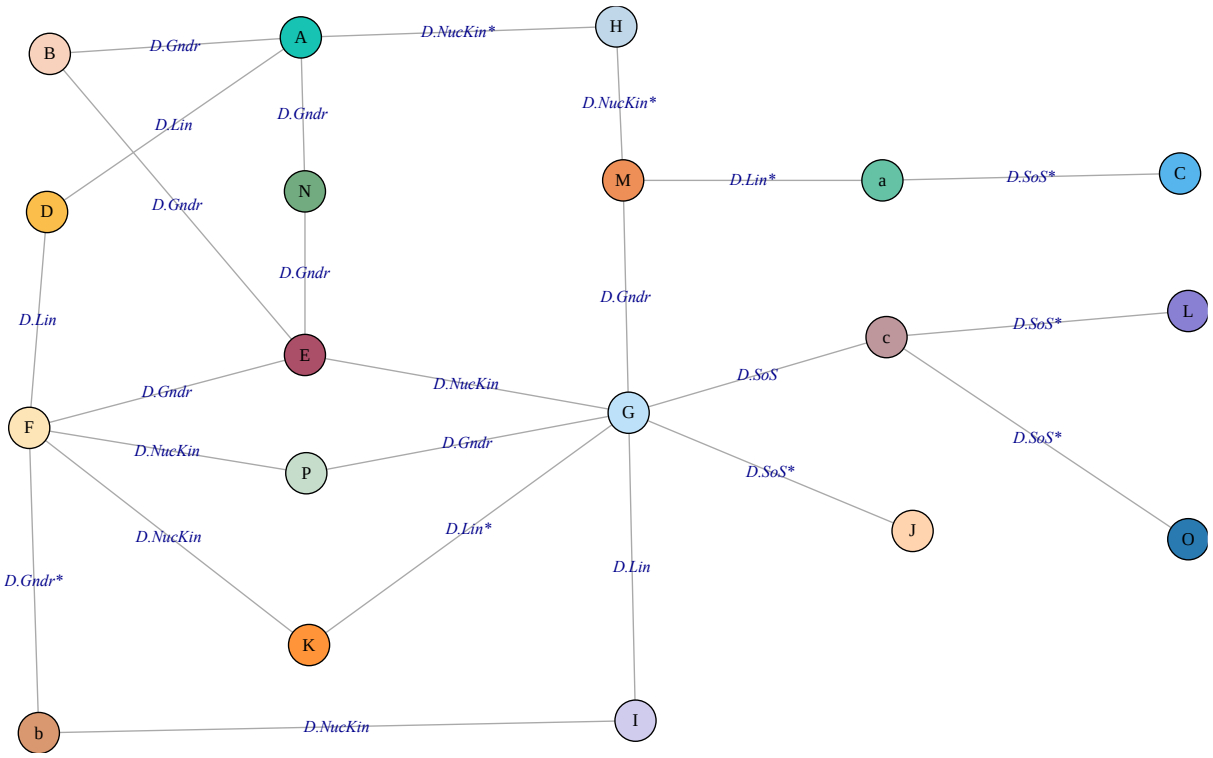


Figure S5.9: Network for the G^{-1} typology. This network contains three unobserved types that are added to ensure the network is fully connected.

Unobserved types

label	Coded description
a	(S BS)(D ZD BD) ZS
b	(S D)(BS BD)(ZS ZD)
c	X //



APPENDIX D

Appendix D: Supplementary Material for Chapter 6

Chapter 6: Kinship & Cooperation

Supplementary Material

Preregistration

All pre-registered materials, including a mock-up of the survey, can be found at this address: https://osf.io/45hdp/

The survey mock-up is similar but not identical to the version seen by participants due to technical and aesthetic restrictions in the implementation of the survey.

Specific differences are:

- Multi-choice answers are listed horizontally as radio buttons, rather than as text.
- Names are not in square brackets in the live study as in the mock-up
- The continuous scale in the mock-up was converted to a 5 points scale
- Inheritance amount was converted to Rupees in the Hindi-Hindi version
- Headings indicating the intent of the section in mock-up are not present.

Odds Ratio results

Table S6.1: In text, odds ratio results are used to determine the size of the preference between a genealogical sister and equal treatment of kin. Here I display this data in table form. All CI are 95%. The predictions are drawn from the 'with Hindi-English' raw response model. Columns in this table show the scenario and language, followed by columns indicating the odd ratio for scoring above 3 (>3) or equal to 3 (=3), and confidence intervals for each of these. Scores of above 3 indicate a preference for a genealogical sister, and equal to three indicate equal treatment of the two relatives. To generate the odds ratio between languages and scenario one takes the ratio of one row (>3 / =3) and divides is against the ratio of another row.

Scenario	Language	>3	>3 lower CI	>3 upper CI	=3	=3 lower CI	=3 upper CI
Babysitting	English	0.285	0.271	0.298	0.673	0.662	0.684
Babysitting	Hindi	0.194	0.183	0.206	0.731	0.722	0.740
Babysitting	Hindi-English	0.358	0.343	0.374	0.613	0.601	0.626
Birthday	English	0.227	0.214	0.239	0.714	0.704	0.723
Birthday	Hindi	0.150	0.140	0.159	0.747	0.739	0.755
Birthday	Hindi-English	0.293	0.279	0.307	0.667	0.655	0.678
CPR	English	0.380	0.364	0.396	0.595	0.583	0.608
CPR	Hindi	0.273	0.259	0.286	0.681	0.671	0.692
CPR	Hindi-English	0.461	0.444	0.478	0.522	0.509	0.535
Inheritance	English	0.448	0.431	0.465	0.535	0.521	0.548
Inheritance	Hindi	0.332	0.318	0.347	0.635	0.623	0.647
Inheritance	Hindi-English	0.531	0.513	0.549	0.457	0.444	0.471
Moving house	English	0.281	0.267	0.294	0.676	0.665	0.687
Moving house	Hindi	0.191	0.180	0.202	0.732	0.723	0.741
Moving house	Hindi-English	0.354	0.339	0.369	0.617	0.605	0.629

All model outputs

Below are the summary outputs for each of the eight models compared in table 1. The main text mostly discussed the table under With Hindi-English, Raw, No interaction, which is also given in the main text as table 2.

Term is the parameter, estimate is the posterior mean estimate, std. error is standard error, and lower and upper and 95% confidence intervals for the estimate. All effects where the 95% CI does not contain zero are in bold.

Models have either 3 or 4 intercepts. These are a function of the ordinal model being implemented, which is approximating an underlying variable, which in this case we might presume is cooperation. A model will have 3 intercepts when modelling the forced-choice response, and 4 intercepts when modelling the raw response. Intercept parameters stand for the cumulative log-odds of each response value, minus 1 (since probabilities add to 1.0 we don't need to calculate the last one). By modelling each response as cumulative odds we guarantee the importance of ordering in the responses is maintained, and account for the frequency of those responses (McElreath 2020).

Without Hindi-English

Table S6.2: Raw response model, excluding Hindi-English participants, without an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.380	0.789	-6.685	-4.148
Intercept 2 – 3	-3.193	0.659	-4.281	-2.132
Intercept 3 – 4	2.012	0.623	1.007	3.069
Intercept 4 – 5	3.892	0.648	2.850	5.012
Hindi-Hindi	-0.696	0.312	-1.197	-0.182
Babysitting	-0.126	0.280	-0.575	0.336
Birthday party	-0.328	0.281	-0.786	0.127
Inheritance	**0.882**	**0.274**	**0.444**	**1.329**
CPR	**0.515**	**0.276**	**0.064**	**0.958**
Gender (M)	0.186	0.313	-0.335	0.684
Age (continuous)	0.020	0.014	-0.003	0.043

Table S6.3: Raw response model, excluding Hindi-English participants, with an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.354	0.811	-6.722	-4.053
Intercept 2 – 3	-3.154	0.664	-4.251	-2.057
Intercept 3 – 4	2.109	0.633	1.083	3.170
Intercept 4 – 5	4.013	0.658	2.973	5.114
Hindi-Hindi	-0.558	0.481	-1.347	0.236
Babysitting	-0.334	0.380	-0.956	0.304
Birthday party	-0.471	0.383	-1.107	0.158
Inheritance	**1.198**	**0.373**	**0.589**	**1.819**
CPR	**0.832**	**0.371**	**0.226**	**1.433**
Gender (M)	0.197	0.311	-0.316	0.718
Age (continuous)	0.020	0.014	-0.002	0.043
H-H: Babysitting	0.470	0.566	-0.469	1.409
H-H: Birthday Party	0.350	0.567	-0.567	1.282
H-H: Inheritance	-0.675	0.556	-1.592	0.227
H-H: CPR	-0.671	0.558	-1.580	0.258

Forced choice

No Interaction

Table S6.4: Forced-choice response model, excluding Hindi-English participants, without an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.736	0.819	-7.134	-4.421
Intercept 2 – 3	-0.604	0.671	-1.698	0.463
Intercept 3 – 4	4.489	0.699	3.317	5.589
Hindi-Hindi	-1.057	0.356	-1.644	-0.470
Hindi-English	0.327	0.482	-0.442	1.154
Babysitting	0.362	0.252	-0.055	0.771
Birthday party	-0.046	0.254	-0.472	0.367
Inheritance	**1.385**	**0.264**	**0.949**	**1.824**
CPR	**0.911**	**0.256**	**0.495**	**1.336**
Gender (M)	0.200	0.341	-0.374	0.743
Age (continuous)	0.024	0.015	-0.001	0.048

Table S6.5: Forced-choice response model, excluding Hindi-English participants, with an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.975	0.882	-7.512	-4.587
Intercept 2 – 3	-1.013	0.711	-2.183	0.159
Intercept 3 – 4	4.128	0.748	2.930	5.370
Hindi-Hindi	-1.246	0.508	-2.106	-0.418
Babysitting	-0.272	0.387	-0.907	0.359
Birthday party	-0.200	0.393	-0.851	0.456
Inheritance	**1.076**	**0.401**	**0.415**	**1.748**
CPR	**1.193**	**0.403**	**0.550**	**1.873**
Gender (M)	0.048	0.364	-0.542	0.653
Age (continuous)	0.021	0.016	-0.005	0.046
H-H: Babysitting	**0.998**	**0.555**	**0.127**	**1.935**
H-H: Birthday Party	0.303	0.568	-0.606	1.252
H-H: Inheritance	0.087	0.571	-0.867	1.034
H-H: CPR	-0.598	0.566	-1.536	0.338

With Hindi English

Table S6.6: Raw response model, including Hindi-English participants, without an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.339	0.783	-6.671	-4.110
Intercept 2 – 3	-3.038	0.660	-4.119	-1.939
Intercept 3 – 4	2.368	0.644	1.335	3.488
Intercept 4 – 5	4.270	0.666	3.205	5.421
Hindi-Hindi	-0.705	0.318	-1.231	-0.208
Hindi-English	0.476	0.416	-0.204	1.145
Babysitting	0.032	0.256	-0.389	0.467
Birthday party	-0.398	0.251	-0.807	0.024
Inheritance	**1.051**	**0.246**	**0.660**	**1.464**
CPR	**0.648**	**0.253**	**0.233**	**1.072**
Gender (M)	0.346	0.306	-0.143	0.866
Age (continuous)	0.023	0.015	-0.001	0.048

Table S6.7: Raw response model, including Hindi-English participants, with an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.440	0.815	-6.766	-4.138
Intercept 2 – 3	-3.099	0.684	-4.242	-1.967
Intercept 3 – 4	2.402	0.672	1.328	3.530
Intercept 4 – 5	4.344	0.697	3.239	5.544
Hindi-Hindi	**-0.577**	**0.493**	**-1.413**	**0.222**
Hindi-English	0.221	0.599	-0.762	1.205
Babysitting	-0.351	0.380	-0.984	0.284
Birthday party	-0.510	0.382	-1.141	0.111
Inheritance	**1.237**	**0.375**	**0.622**	**1.858**
CPR	**0.867**	**0.371**	**0.260**	**1.488**
Gender (M)	0.329	0.304	-0.161	0.835
Age (continuous)	0.024	0.015	0.000	0.049
H-H: Babysitting	0.489	0.558	-0.424	1.401
H-E: Babysitting	0.970	0.670	-0.117	2.083
H-H: Birthday party	0.380	0.572	-0.583	1.321
H-E: Birthday party	-0.199	0.691	-1.323	0.931
H-H: Inheritance	-0.694	0.554	-1.608	0.200
H-E: Inheritance	0.428	0.661	-0.614	1.523
H-H: CPR	-0.689	0.548	-1.610	0.204
H-E: CPR	0.182	0.674	-0.905	1.315

Forced choice

Table S6.8: Forced choice response model, including Hindi-English participants, without an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-5.867	0.858	-7.331	-4.515
Intercept 2 – 3	-0.647	0.684	-1.778	0.465
Intercept 3 – 4	4.459	0.725	3.299	5.671
Hindi	-1.094	0.361	-1.686	-0.509
Hindi-English	0.305	0.460	-0.448	1.065
Babysitting	0.364	0.252	-0.039	0.781
Birthday party	-0.041	0.250	-0.452	0.370
Inheritance	**1.398**	**0.260**	**0.975**	**1.818**
CPR	**0.918**	**0.261**	**0.480**	**1.342**
Gender (M)	0.199	0.324	-0.332	0.727
Age (continuous)	0.024	0.016	-0.001	0.050

Table S6.9: Forced-choice response model, including Hindi-English participants, with an interaction term

term	estimate	std.error	lower	upper
Intercept 1 – 2	-6.091	0.917	-7.626	-4.622
Intercept 2 – 3	-0.810	0.741	-2.036	0.378
Intercept 3 – 4	4.472	0.770	3.228	5.736
Hindi	-1.245	0.515	-2.088	-0.419
Hindi-English	-0.183	0.654	-1.280	0.886
Babysitting	-0.264	0.393	-0.912	0.365
Birthday party	-0.193	0.383	-0.833	0.435
Inheritance	**1.144**	**0.401**	**0.494**	**1.795**
CPR	**1.242**	**0.398**	**0.602**	**1.898**
Gender (M)	0.213	0.343	-0.342	0.769
Age (continuous)	0.024	0.017	-0.003	0.051
H-H: Babysitting	**1.007**	**0.568**	**0.071**	**1.944**
H-E: Babysitting	**1.304**	**0.708**	**0.152**	**2.503**
H-H: Birthday party	0.309	0.555	-0.595	1.231
H-E: Birthday party	0.168	0.700	-0.973	1.311
H-H: Inheritance	0.057	0.569	-0.863	0.987
H-E: Inheritance	**1.560**	**0.732**	**0.326**	**2.755**
H-H: CPR	-0.633	0.570	-1.585	0.295
H-E: CPR	-0.231	0.720	-1.414	0.969

APPENDIX E

Appendix E: Usage frequency and lexical class determine the evolution of kinship terms in Indo-European

I am joint first-author on this paper. My contributions were to collate the kinship data, program the automated cognate coding, estimate the phylogenetic rates of change, and contribute to the writing of the manuscript and supplementary material.

This paper looks at whether kinship terminology, as a system of words, follows the evolutionary and linguistic principle that rates of change are negatively correlated to usage. Our study of Indo-European languages finds that kinship terminology follows this trajectory: more frequently used kinship terms are less likely to change than less frequently used terms. Above this general principle, we find that frequently used kinship terms are less likely to change than basic vocabulary words that are used as frequently, and that less frequently used kinship terms are more likely to change than basic vocabulary words that are used at a similar frequency. Secondly, we find that frequently used terms tend to be closer genealogical relatives (e.g. M, F), and less frequently used terms are more distant (e.g. MZ, MB).

The results from this paper highlight that, while kinship terminology act according to this linguistic principle, the relationship between kinship terms creates modular patterns of change. Within Indo-European languages, the nuclear family terms are connected; and parent's siblings, and parent's siblings children are connected. As such they are seen to change in a modular fashion.

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Author for correspondence:
Péter Rácz
e-mail: raczp@ceu.edu

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Usage frequency and lexical class determine the evolution of kinship terms in Indo-European

Péter Rácz[1,2], Sam Passmore[2], Catherine Sheard[3,4] and Fiona M. Jordan[2]

[1]Cognitive Development Center, Central European University, Budapest 1051, Hungary
[2]Department of Anthropology and Archaeology, University of Bristol, Bristol BS8 1UU, UK
[3]School of Biology, University of St Andrews, St Andrews KY16 9TJ, UK
[4]School of Earth Sciences, University of Bristol, Bristol BS8 1TQ, UK

PR, 0000-0001-7896-4801; SP, 0000-0002-5302-356X; CS, 0000-0002-8259-1275; FMJ, 0000-0002-9953-8884

Languages do not replace their vocabularies at an even rate: words endure longer if they are used more frequently. This effect, which has parallels in evolutionary biology, has been demonstrated for the core vocabulary, a set of common, unrelated meanings. The extent to which it replicates in closed lexical classes remains to be seen, and may indicate how general this effect is in language change. Here, we use phylogenetic comparative methods to investigate the history of 10 kinship categories, a type of closed lexical class of content words, across 47 Indo-European languages. We find that their rate of replacement is correlated with their usage frequency, and this relationship is stronger than in the case of the core vocabulary, even though the envelope of variation is comparable across the two cases. We also find that the residual variation in the rate of replacement of kinship terms is related to genealogical distance of referent to kin. We argue that this relationship is the result of social changes and corresponding shifts in the entire semantic class of kinship terms, shifts typically not present in the core vocabulary. Thus, an understanding of the scope and limits of social change is needed to understand changes in kinship systems, and broader context is necessary to model cultural evolution in particular and the process of system change in general.

1. Background

Languages change over time: sounds, syntax and vocabulary are all in varying states of flux due to the shifting social equilibrium

in which language users interact. Innovations arise in populations, and variants undergo filtering processes that determine their rise or fall in the long run. Older views of language evolution saw these processes as a force of nature, severed from and unaffected by the dynamics of the speaker community [1], but those perspectives have been largely replaced by work in variationist sociolinguistics [2] and usage-based linguistics [3] which relate language change to social and cognitive biases in the individual and patterns in the community.

Sociolinguistic research that focuses on the individual-level aspects of how language is learned and transmitted in the community [4,5] is mirrored by a predominantly micro-evolutionary [6,7] approach to human social learning in general [8,9]. This approach has a primary focus on modelling the dynamics of cultural variation within populations by considering the effects of biased social learning on the fate of cultural features, either due to their inherent properties (content), or aspects of the transmission process (context) [8].

The relationship between micro- and macro-evolutionary dynamics of cultural evolution is still not well understood: for example, what generalities can be made in how changes in speaker behaviour ramify up to differences between languages? Historical linguistics has increasingly drawn on the theory and methods of evolutionary biology to provide macro-evolutionary frameworks for understanding and analysing patterns of language relatedness, diversification and change. Phylogenetic inference of large-scale language family relationships is increasingly commonplace [10] due to the development of quantitative models appropriate for lexical replacement [11]; in turn, analysts are able to estimate dates of diversification and age of origin of related languages [12–14] without assuming that language changes at constant rates.

Phylogenetic methods have also demonstrated that the rate of replacement in the core vocabulary of a language correlates with its usage frequency in large-scale linguistic corpora [15]. The core vocabulary is a predefined set of frequent words such as 'heart', 'walk', 'bone' and 'good' [16]. For example, while German retains the Proto-Germanic form for 'chair', 'Stuhl', English has replaced it with the Latin form, probably as a result of rising Franco-Norman influence in the language's history. However, both German and English retain the Proto-Germanic form for 'man', which is a much more frequently used term than 'chair' and a part of the core vocabulary. This so far appears to be a robust correlation, as words for more frequently used meanings are replaced at a slower rate in core vocabulary [15] and in numerals [17], prompting the claim that frequency of usage could provide a cross-linguistic general mechanism for the rate differences in lexical replacement [15]. An analogous process exists in biological evolution, where highly conserved (slowly evolving) regions of genetic material are generally considered to have increased functional utility in biological processes compared with faster-evolving regions [18].

In language, the mechanisms responsible for the shielding effects of frequency of use remain unclear. While language change ultimately occurs at the individual level, it is very unlikely that a word's frequency of occurrence in a particular language's corpora maps directly onto its rate of replacement for several reasons. The two factors operate on different time-scales, frequency of occurrence is at best an indirect measure of the strength of a word's lexical representation [19], and word frequencies are themselves correlated within a language corpus [20,21]. This is an especially pertinent aspect of words in closed classes of content words (such as number or colour systems), where the universe of potential meanings and referents is relatively restricted, because a change in one part of the system may have knock-on effects that ramify throughout [22,23].

In most descriptions, the terminology of open/closed and content/function are used interchangeably for word classes. Here, we step away from this and use 'closed semantic class' to refer to a set of closely related words where the head words can be listed exhaustively. By contrast, an open semantic class has loose (if any) connections between its members and can theoretically be of any size.

Human kinship is an extensively studied example of a closed semantic class; specifically, the terminological (lexical) systems used to refer to relatives [24]. Kinship terminologies are cultural as well as linguistic phenomena, reflecting a society's wider social norms governing relatedness, marriage, inheritance and family organization. Despite a breadth of diversity in social norms, kinship terminologies show far less variation than is combinatorially possible. This lack of diversity is at least partially constrained by our biological inheritance as social primates [25,26], but equally by cognition [27] and strong patterns of cultural inheritance [28]. Kinship terminologies provide us with a platform to explore the interaction of biological and cultural domains, and their effect on language use and change [29].

Kinship words together constitute systems in the sense that they have a culturally circumscribed range of referents (individuals are or are not kin; if so, are different kinds of kin). Importantly, they pattern together. For example, Swedish distinguishes *father's father* and *mother's father*, and Polish distinguishes *sister's daughter* and *brother's daughter*, while English makes no such contrasts: those

Table 1. Kinship terms for father's father (FF), mother's father (MF), sister's daughter (ZD) and brother's daughter (BD) in Swedish, Polish and English.

	Swedish	Polish	English
FF	*farfar*	*dziadek*	*grandfather*
MF	*morfar*	*dziadek*	*grandfather*
ZD	*syster-dotter*	*siostrzenica*	*niece*
BD	*brors-dotter*	*bratanica*	*niece*

relatives are, respectively, grandfathers and nieces. When a kinship system changes, words are replaced in clusters: a shift from a Swedish-type system to an English-type system could erase *both* the term for *father's father* and for *mother's father* (table 1).

This means that a kinship term might be replaced in itself, but this change will tend to propagate over the range of related terms. The rate of replacement for a given term is determined by shifts in the entire semantic class rather than by the frequency of the term itself.

The replacement of the semantic class, while ultimately contingent on usage frequency (words no longer said will disappear), is subject to complex social and cultural pressures [28,30]. Typological work suggests that kinship changes on the level of entire semantic classes rather than individual words, but the patterns of change in form and meaning in kinship terminologies are far from systematically surveyed (see [31]). The aim of this work is to address this issue in kinship research and thereby to shed light on how frequency effects in language change are mediated by semantic classes.

2. Questions

The rate of replacement of the Indo-European core vocabulary, a set of frequent words like 'heart', 'walk', 'bone' and 'good' that constitute an open semantic class, correlates with their usage frequency [15]. In this paper, we use phylogenetic comparative methods to analyse kinship words in Indo-European and address the following questions. (i) Do kinship words show the same effect of usage frequency on the rate of replacement as core vocabulary words? That is, can frequency effects on the core vocabulary be replicated with a closed semantic class? (ii) Given that kinship words are argued to shift together as a class rather than individually and incrementally, does this result in a difference between the effect of usage frequency for core vocabulary words and for kinship terms?

3. Methods

To address these questions, we selected a set of widely shared kin categories and collected the terms used for those kin-types in 47 Indo-European languages. We then sampled the word usage frequencies of each kin term in a range of corpora from a subset of those languages (mostly from Europe) and determined the rate of replacement for each term to compare replacement rate and usage frequency, following earlier work on the core vocabulary [15].

Data were collected for ten basic consanguineal kin term categories. The categories cover parents, children, siblings, aunts/uncles and cousins, while the languages represent five main branches of Indo-European.

We then generated cognate classes for the specific forms across the language sample and paired these with a phylogeny of Indo-European languages to determine the rates of replacement for the individual terms. This allowed us to estimate the rate of replacement for each basic kin term category. We followed similar work on the core vocabulary that used the 200-item Swadesh list [16], a compilation of fundamental lexicalized concepts used in comparative linguistics. This practice works at a greater resolution and consequently entails a higher level of specificity than specifying cognate historical relationships. For instance, we consider German 'bruder' and French 'frére' as members of two different cognate classes given both their formal and etymological distance.

Figure 1 shows the classes in colour for the words expressing mother's sister (MZ) and brother (B) in our dataset across languages in the Indo-European family tree. The types of terms used for MZ are more diverse than those used for B; taking into consideration the genealogical history of these terms, we can

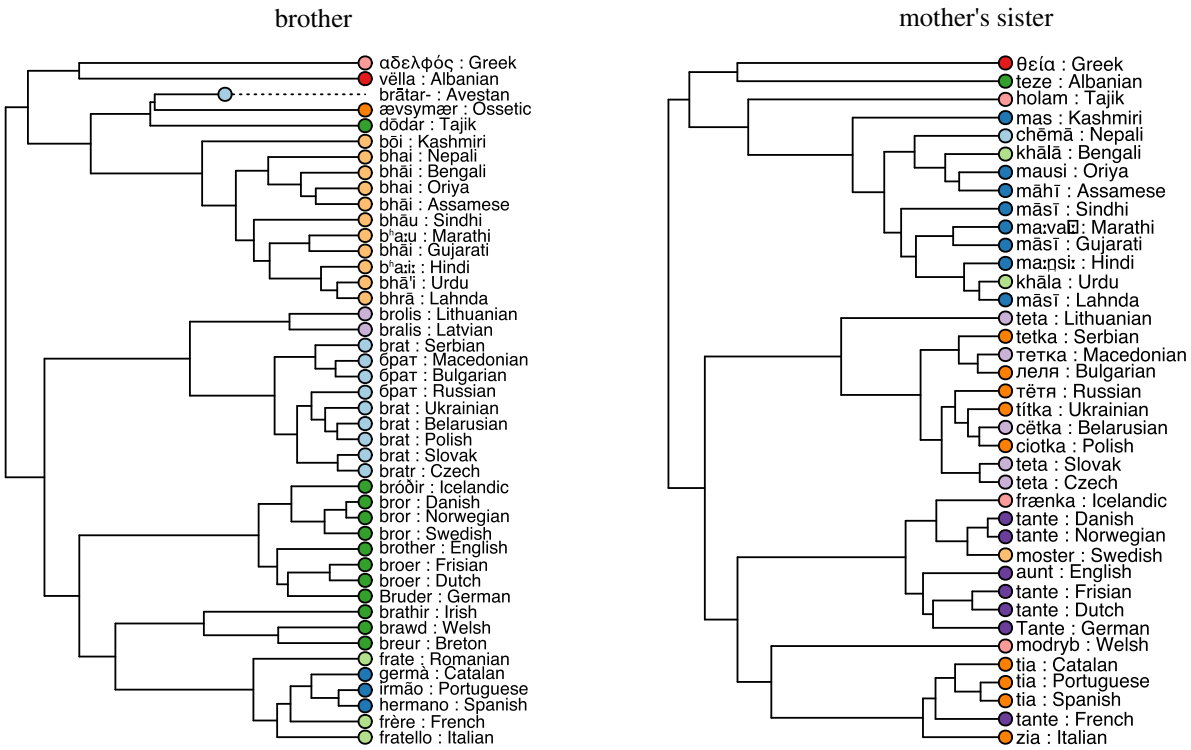

Figure 1. The Indo-European phylogeny and cognate classes (indicated by colour) derived by LingPy and checked by linguists for the terms brother and mother's sister (aunt).

estimate that this difference in diversity stems from the fact that B terms are replaced slower than MZ terms on a historical time-scale.

The rate of replacement estimates were then compared with frequency of use across corpora.

3.1. Kinship data

As part of a larger database project on kinship terminology, we collected kin terms from 47 languages for the following relatives: brother (B), daughter (D), father (F), mother (M), maternal uncle (MB), maternal aunt (MZ), maternal aunt's daughter (MZD), maternal aunt's son (MZS), son (S) and sister (Z). Most Indo-European languages do not distinguish lineal relationships with separate terms, such as maternal versus paternal uncle (e.g. MB versus FB), and if they do such terms tend to be rare in contemporary kinship terminologies. Therefore, we used terms for maternal relatives as representative. We have not included words for spouses (e.g. husband or wife), because these are often the same word as 'man' or 'woman'. Frequency data were collected from 34 corpora in 21 languages in three corpus types: spoken, written and web-crawled. The sources for the terms and the corpora are listed in the electronic supplementary material.

3.2. Cognate data

We generated cognate classes by using the Indo-European Etymological Dictionary [32], LingPy [33] and expert judgement, inviting volunteers on Linguist List to review the cognate classes. All terms were first automatically transcribed into the Speech Assessment Methods Phonetic Alphabet (SAMPA) through LingPy's `uni2sampa` function. Cognates were automatically allocated using LingPy's cluster function with an edit-distance algorithm and 0.4 threshold. These categories were then reviewed by expert volunteers. Automatic decisions and expert corrections are available in the electronic supplementary material. To compare kinship terms with basic vocabulary, we obtained measures of frequency and rates of replacement for meanings on the Swadesh list. Measures for frequency of use in Swadesh terms for English, Spanish, Russian and Greek, and the rates of replacement for Indo-European languages for Swadesh terms were obtained from the electronic supplementary material of [15], which we follow in our methods. Measures for frequency of use in Swadesh terms for Portuguese, French, Czech, Polish and German come from the electronic supplementary material of [34].

3.3. Phylogeny

To estimate rates of replacement and to account for phylogenetic uncertainty, we used 1000 phylogenies from the most recent Bayesian posterior of Indo-European phylogenies [13]. Trees in the sample are rooted. Branch lengths are given in years and derived from statistical and historical calibration, which dates Proto-Indo-European to approximately 8700 years ago. Trees initially have 111 taxa, and these were pruned for each kin term to match the available data.

3.4. Rates of replacement

Following the methods in [35], we used BayesTraits v. 3.0.1 to implement a phylogenetic Bayesian MCMC approach to estimate the instantaneous global rate of replacement for each kin term through Q-matrix normalization. Probabilities of frequency were scaled to represent the empirical frequencies. We used a stepping-stone sampler, using 100 stones for 1000 iterations each. MCMC chains run for a total of 10 010 000 iterations, with a burn-in of 10 000, sampling every 1000. This leaves a posterior sample of 10 000 iterations (approx. 10 iterations per tree). To make the rates comparable to previous work, we scaled instantaneous rates to change per 10 000 years. For each kin term, we ran MCMC chains three times, to ensure convergence. The averaged results of each run, as well as Gelman–Rubin diagnostic tests of MCMC-chain convergence are available in the electronic supplementary material [36].

3.5. Usage frequency and rates of replacement

We used the lme4 package in R [37,38] to fit a mixed-effects generalized logistic regression model to the combined data (basic vocabulary and kinship terms). The outcome variable is the mean rate of replacement estimated for a word meaning. The predictor variables are aggregated centralized log frequency per million (clfpm) per word per language and word type (Swadesh term or kin term). Swadesh terms that are kin terms (mother, father, husband and wife) were excluded (for details, see the electronic supplementary material).

The random effect structure of the reported model was selected using model comparison based on goodness-of-fit tests and the Akaike information criterion.

4. Results

Our main questions were (i) whether kinship words show an effect of usage frequency on the rate of replacement and (ii) whether this effect is different for kinship words and words in the core vocabulary. In order to answer these questions, we modelled the rate of replacement of ten kin terms in Indo-European and, in turn, compared (i) the rates of replacement to the frequency of use in language corpora and (ii) our kin term data with available data on core vocabulary terms.

We found a negative correlation between how often a kin term is used in the languages in our sample and its estimated rate of replacement (est = −0.58, s.d. = 0.07, $t = -8.72$). Genealogically close terms like 'mother', 'sister' or 'son' are used more frequently and change slower. By contrast, more distant terms like 'mother's sister' (English: 'aunt', French: 'tante', etc.) are less frequent and change faster. In this respect, kin terms behave like core vocabulary: more frequent terms change slower in linguistic evolutionary history.

Figure 2 shows the log frequency distribution of our terms across the languages in the sample (x-axis). The terms themselves are sorted according to their estimated rate of replacement. Mother's (or father's) sister (MZ), which has the highest estimated rate of replacement, is on top. Brother (B), which has the lowest rate, is at the bottom. While the relationship is not uniform, we see that, overall, terms that are used more frequently are also replaced slower across languages.

In addition, this relationship between frequency of use and replacement is *stronger* for kin terms than for general vocabulary terms (est = 0.18, s.d. = 0.09, $t = 2.02$). Kin terms used more frequently change slower, while those used less frequently change faster than terms in the core vocabulary. This can be seen in figure 3, which shows the mean log frequencies (x-axis) of kin terms (red labels) and Swadesh terms (grey points) across their mean rate of replacement (y-axis). The regression line expressing the strength of the correlation is steeper for kin terms than for Swadesh terms. The envelope of variation for kin terms and core vocabulary is similar. Since kin term frequencies were sampled from a range of

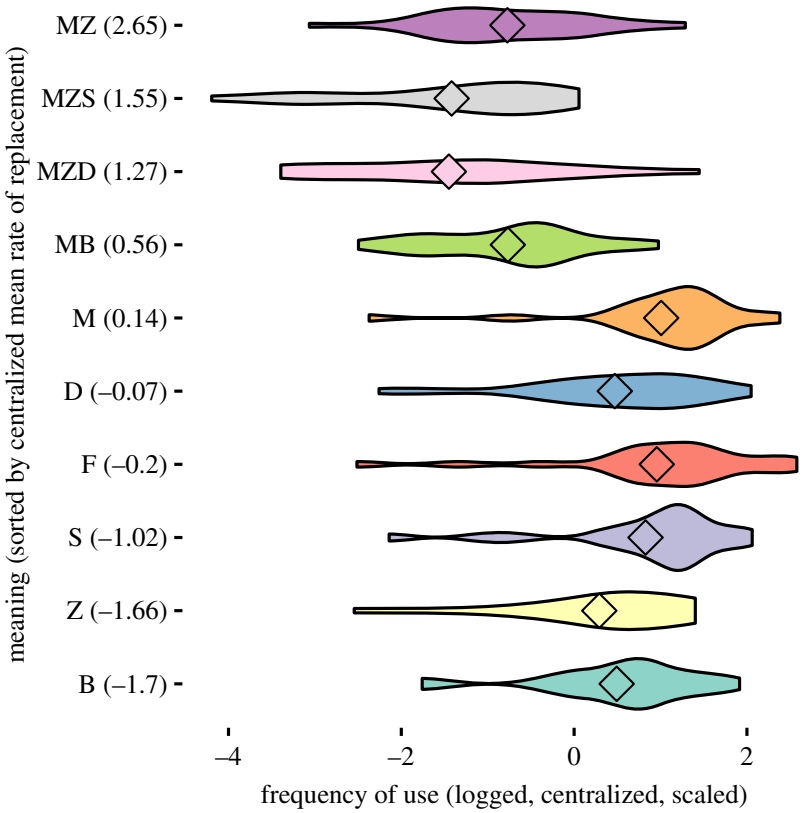

Figure 2. Usage frequency across languages for kin terms in the data (sorted by the term's mean rate of replacement).

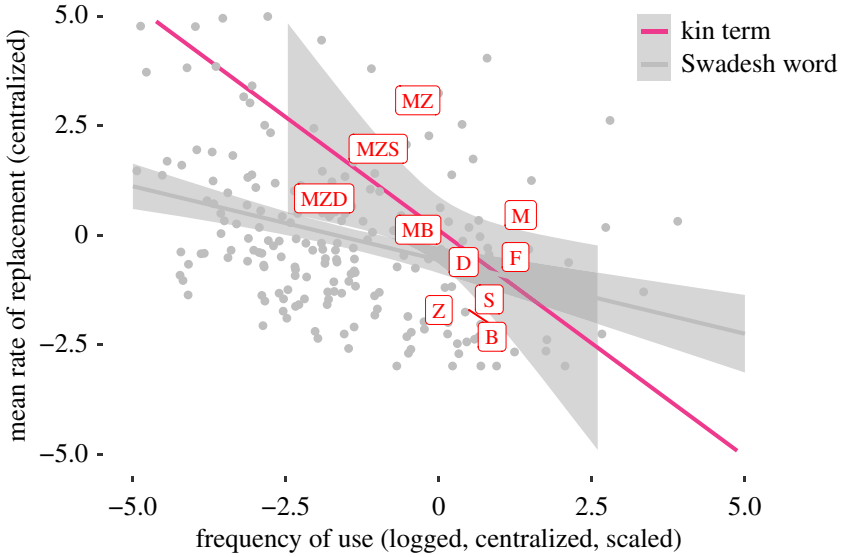

Figure 3. The relationship between the mean rate of replacement and the mean usage frequency for Swadesh words (grey) and kin terms (red), with a simple linear model.

corpora (encompassing different registers, *viz*. written, spoken and web-based language), this remains a robust result.

In sum, kin terms resemble the general vocabulary in that respective words used more frequently are more resistant to being replaced. This effect is more drastic for kin terms, which are even less likely to be replaced when they are frequent and even more likely when they are rare, in comparison with the core vocabulary.

5. Discussion

The idea that closed lexical classes vary in their rate of replacement has received attention [35]. Yet, to our knowledge, ours is the first study that systematically investigates the behaviour of a closed semantic class in comparison with an open class (the items of the core vocabulary) using corpus data and phylogenetic methods.

Our results indicate that a closed semantic class is not simply more or less volatile than an open semantic class in this regard. The systematic difference in the strength of the interaction between frequency and rate of replacement potentially stems from the nature of change in kinship systems. Changes may be concerted and systematic over a category of relatives, rather than independently replacing words one by one. This, in turn, is because kinship systems incorporate conceptual reflections of real-life social structures of family and kinship, and they are affected by changes in social conditions, societal norms and inheritance. For example, the Latin kinship system distinguished paternal uncles (FB, *patruus*) from maternal (MB, *avunculus*); towards the end of the Roman republic; however, *avunculus* was being used bilaterally, with similar changes occurring in parent's sister and cousin terms [24]. These linguistic changes are argued to reflect the rise of a religious belief in monogamy, nuclear-family focused peasantry and restrictions on degrees of allowed marriage.

The peculiar evolution of kinship terms is therefore not an idiosyncratic quality, but rather one to be explained through the details of the process. When we look at Indo-European kinship, we see that often-invoked filial (brother, sister) and spousal (wife, husband) terms change rarely.

More distant consanguineal terms are more prone to shifts, including levelling scenarios where terms may sweep over previously differentiated relatives. One example is the rise of 'cousin' and its minor variants (German 'Cousin/e', French 'cousin/e', Polish 'kuzyn/ka') to cover all parents' siblings children across Europe (visible in our data); cross/parallel distinctions were previously attested in different branches of Indo-European [39].

The more abrupt and wider changes in semantic systems neatly account for the observed behaviour of kinship terms in our sample. Core terms, like 'father' and 'daughter' are replaced disproportionately slower, because semantic shifts between kinship systems are less likely to affect these terms. By contrast, more distant terms, like 'aunt' and 'cousin', are replaced in such shifts more often. While we need to speculate at this point, it is ultimately also likely that age of learning ('mother' learned earlier than 'aunt') and frequency of use play a role here [40].

One caution needs to be raised due to the atypicality of the Indo-European language family. It is no accident that globally, language corpora and phylogenetic information are most readily available for Indo-European languages. These are mostly spoken in industrialized nation-states with a long history of language documentation and scholarly attention. Recent research [41] argues that shifts in European kinship, spread via the Christian Church in the Middle Ages, promulgated democracy and industrialization in Europe. If this is the case, we may be able to study language change in these populations indirectly because of kinship dynamics; however, the effect may be on the generality of these results rather than a bias in outcome.

More broadly, our sample of Indo-European languages over-represents WEIRD (Western, educated, industrialized, rich, democratic) societies [42] as well as so-called Eskimo bilateral kinship systems [43] and thus limits generality. Across Europe we also find a strong correlation between genealogical relatedness and geographic distance (siblings live closest, grandparents or grandchildren live a little further, and first cousins live furthest; [44]). This is unlikely to be a global cross-cultural pattern, but exemplifies the relationship between social organization and kinship terminologies.

Recent work [45] has considered the relationship between kinship terms and fitness interdependence, which is the degree to which organisms influence one another's evolutionary fitness, and goes beyond the standard coefficients of relatedness. This work predicts that 'Eskimo' systems in particular will be found where there are strong differentials in the fitness interdependence of 'nuclear' family members versus other relatives, which is in line with the exaggerated relationship we find in the lexical frequency–change relationship. 'Eskimo' systems, in particular, tend to have a smaller kin term inventory than systems that make more distinctions, for example, 'Sudanese'. Inventory size might mediate the ability to detect any frequency–change relationship, and this could be tested if corpora were available for a wider range of languages. We encourage investigations of usage frequency, lexical classes and word evolutionary rates in other language families.

On a more general note, historical linguists can find comfort in our results, which provide additional support to the use of the core vocabulary to establish a correlation between frequency of use and rate of replacement. However, these results also indicate that closed semantic classes behave differently and so across-the-board treatments of language change result in a loss of valuable resolution. The distinctness of kinship terms probably generalizes to other closed classes. This invites further cross-linguistic research on word frequency and language change in other classes, such as colours or numerals [23,46].

In this paper, we used a phylogenetic analysis of kinship words in Indo-European languages to show that for kinship terms, cultural macro-evolutionary patterns are partially mediated through exaggerated frequency effects. The creative analogy of parallels between biological and cultural evolution is

heuristically valuable and opens up a diverse hypothesis space for unique aspects of human culture such as kinship. The replacement rate of genes, like that of words, is at least partially dependent on their function [18]. Anthropologists and linguists hold rich resources of empirical data that can be used to elaborate the operationalization of 'cultural transcription'. Here, we have drawn on different genres of language corpora for usage frequency: web corpora, in particular, provide access to a wide range of naturalistic language at much less cost than curated national corpora. Furthermore, classes of traits that evolve in concert, and particular phenotypes (or traits) that are more or less likely to arise due to properties of the system as a whole, are phenomena that occur across evolving systems: biological processes of evolvability [47] and developmental bias [48,49] could provide useful analogies for future research.

Our results that changes within semantic classes are correlated at the macro-evolutionary scale and thus that cultural context can constrain language change, emphasize the need for careful application of the appropriate evolutionary methods to the study of cultural evolution.

Data accessibility. All our data and code are available in the extended electronic supplementary material hosted at doi:10.5281/zenodo.3453517.

Authors' contributions. P.R., S.P., C.S. and F.M.J. designed research; P.R. collected corpus data; S.P. and F.M.J. collected kinship terms; S.P. and C.S. performed phylogenetic analyses; P.R. performed regression analysis; P.R. wrote the first draft of the manuscript and S.P. the first draft of the electronic supplementary material, with all authors contributing writing and editing. P.R. and S.P. contributed equally to this work.

Competing interests. We declare we have no competing interests.

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APPENDIX F

Appendix F: Social Practice and Shared History, Not Social Scale, Structure Cross-Cultural Complexity in Kinship Systems

My contribution to this paper was performing the phylogenetic signal testing, as well as assisting in the development of the ordinal model, in writing the paper, and in creating the figures.

This paper highlights the relationship between kinship terminology and social structure, while ruling out a confounding effect of population size or social complexity. By ruling out the relationship between population size and social complexity as influences on kinship terminology, we highlight the diversity in societal evolution cross-culturally.

Here, the results showed that patterns of marriage, and patterns of descent, are correlated with an ordinal response variable where 1 indicates a Hawaiian-style terminology and 4 is a Sudanese-style terminology (see figure 1 in this paper). Specifically, this model highlights the prohibition of cousin marriage in a Hawaiian-style terminology (not found in chapter 2, table 2.1), and a flexibility of descent patterns under a Hawaiian-style terminology (which somewhat aligns with results in chapter 2, table 2.1).

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Social Practice and Shared History, Not Social Scale, Structure Cross-Cultural Complexity in Kinship Systems

Péter Rácz,[a,b] Sam Passmore,[b] Fiona M. Jordan[b]

[a]*Cognitive Development Center, Central European University*
[b]*Evolution of Cross-Cultural Diversity Lab, Department of Anthropology and Archaeology, University of Bristol*

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Abstract

Human populations display remarkable diversity in language and culture, but the variation is not without limit. At the population level, variation between societies may be structured by a range of macro-evolutionary factors, including ecological and environmental resources, shared ancestry, spatial proximity, and covarying social practices. Kinship terminology systems are varying linguistic paradigms that denote familial social relationships of kin and non-kin. Systems vary by the kinds of salient distinctions that are made (e.g., age, gender, generation) and the extent to which different kinds of kin are called by the same term. Here, we explore two kinds of explanations for an observed typology of kin terms for cousins. The first one derives the typology from a learning bottleneck linked to population size. This would lead to a correlation between community size and the type of kinship system. The second one derives it from a set of social practices, particularly marriage and transfer of resources that might shape kinship systems. Using a global ethnographic database of over a thousand societies, we show that marriage rules and shared linguistic affiliation have a significant influence on the type of kinship system found in a society. This remains true if we control for the effect of spatial proximity and cultural ancestry. By combining cognitive and historic approaches to this aspect of kinship, we suggest broader implications for the study of human social cognition in general.

Correspondence should be sent to Péter Rácz, Cognitive Development Center, 9 Nádor utca, Central European University, 1051 Budapest, Hungary. E-mail: raczp@ceu.edu

Keywords: Kinship terminology; Social cognition; Semantics; Cross-cultural analysis; Cultural evolution

1. Background

Social and cultural systems of meaning—such as grammatical categories, marriageable partners, the classifications of the natural world, and religious beliefs—all vary across cultures. While these systems are the products of generations of individuals interacting, they also partly reflect the possibilities of the human mind.

Anthropologists have long recognized the adaptive diversity of human behavior and cognition, and the importance and challenge of incorporating the facts of diversity is now an invigorated concern within the cognitive sciences (Evans, 2010; Henrich et al., 2010; Song et al., 2009). Investigations in domains such as color, space, and the body reveal that perception and expression of conceptual categories varies cross-culturally (e.g., Malt & Majid, 2013). At the same time, there are systematic cross-cultural regularities in category structures which may relate to shared human physiology of perception (for example in color categories, see Regier & Kay, 2009). Furthermore, for some domains, cross-cultural variation in categories can be limited by the need for social coordination between individuals (Boyd et al., 1997). Cognitive constraints may also influence the extent to which any categorical system is free to vary (Kemp & Regier, 2012). A strong case can also be made for the mediating effect of cultural evolutionary processes on category formation. These include shared ancestry of language and culture, processes of diffusion and contact (Dunn et al., 2011; Levinson, 2012), as well as co-dependencies between cultural categories and aspects of social and ecological environments (Botero et al., 2014).

A long-standing focus in cognitive anthropology has been the semantic system of *kinship*: how different cultural groups classify family members using language. In this paper, we explore the interaction of culture and cognition by examining the effects of various cultural characteristics on the structure of kinship terminology systems in a large cross-cultural sample.

A core example of cognitive effects on cultural evolution comes from recent work which has pointed to the role of speaker group size in shaping linguistic interaction, and, in turn, the complexity of grammar and vocabulary in language (see e.g., Nettle, 2012). These results indicate that languages spoken by large groups will have larger vocabularies of content words (like verbs and nouns) and less complexity in their morphology (so that fewer function-form pairings of the same word exist). If we can arrange kinship systems along some particular axis of *complexity*, we have predictions on its correlation with the size of the speaker group.

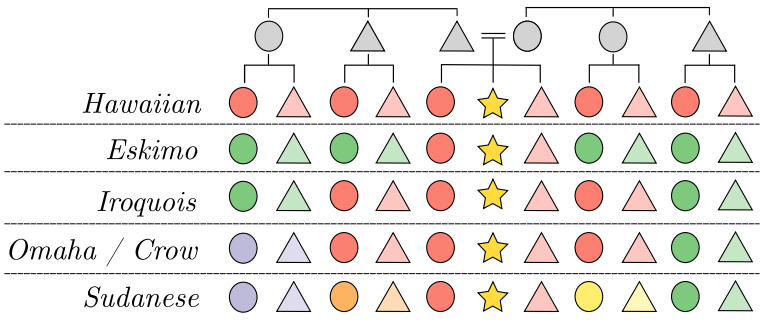
Alternatively, measures of kinship vocabulary complexity may also be shaped by social practice. The complexity of a kinship system is shaped by its roles as a symbolic system interacting with how practices of family and marriage are organized in a society. These practices, and their instantiation in the meanings of words, may then be largely constrained by shared history as language is transmitted over time.

There is evidence for both group size and social practice affecting language in general and social practice affecting kinship terminology in particular. Our paper breaks new ground in that it compares the effects of group size and social practice on kinship terminology. We intend to demonstrate how a complete understanding of the micro-level cognitive processes underlying any semantic category system must also be examined in the macro-level context of cultural history. Some of our cognitive capacities or "gadgets" may themselves be products of a cultural evolution (Heyes, 2018). Similarly, we propose that the adaptive landscape of human social diversity constrains the kinds of social learning our cognitive mechanisms should be equipped to deal with.

1.1. The semantic typology of kinship variation

A kinship terminology system is a cognitive and social category system that is used by speakers of a language to refer to, group together, and distinguish, family members. These terminology sets (here, "kinship systems") vary cross-linguistically in structured and constrained ways (Murdock, 1949). Attested kinship systems show parallels with other category systems like color terms; they reflect cognitive pressures in displaying a trade-off between simplicity and the ability to discriminate. Multiple relatives can be grouped together under one term: for example, an English "aunt" can refer to one's mother's or father's sister. Globally, these extension patterns cover no more than a small space of all possible arrangements (Kemp & Regier, 2012): No language uses the same word to exclusively refer to all one's grandparents and all one's younger siblings.

Typological systems that categorize kinship terminology according to some axes of variation were first named by Morgan (1871). Morgan's typology focuses on the ways in which relatives in own's own (one) generation were named. The systems that he identified and that Murdock (1949, p. 67) later formalized are attached to the contemporary



$$[siblings] < \begin{bmatrix} siblings \\ cousins \end{bmatrix} < \begin{bmatrix} siblings \\ cross\ cousins \\ parallel\ cousins \end{bmatrix} < \begin{bmatrix} siblings \\ cross\ cousins \\ parallel\ cousins \\ maternal\ cousins \\ paternal\ cousins \end{bmatrix}$$

Fig. 1. *Above*: Visual descriptions of the kinship typology. Circles indicate women, triangles indicate men, and the star represents the ego. Colors indicate common terms. *Below*: Increase in cousin term paradigmatic complexity

ethnonyms of paradigm anthropological example communities: Eskimo, Crow, Omaha, Sudanese, Hawaiian, and Iroquois (Fig. 1). Further variations have been identified (e.g., Dravidian, Kachin) and other typological schemes for classifying kinship terminologies proposed, in particular those that concentrate on the terms applied to relatives in one's parental generation (for discussion, see Parkin, 1997). Here, we take advantage of the large body of literature that has explored the Morgan–Murdock typology of kin terms for *cousins* and concentrate on these semantic typologies and their global distribution.

Systems of cousin terms can be ranked according to their paradigmatic complexity, that is, the number of distinctions they envelope in a single form. *Hawaiian* kinship systems use the same words to describe Ego's siblings and the children of Ego's parents' siblings. All relatives in Ego's generation are therefore called by sibling terms. *Eskimo* systems introduce a distinction between *siblings* and *cousins*: most major European languages such as English belong to this category, as do many in South-east Asia. *Iroquois* systems further discriminate parallel cousins (i.e. children of parent's same-sex siblings, such as father's brother's son) and cross-cousins (children of parent's opposite-sex siblings, such as mother's brother's son). *Crow* and *Omaha* systems introduce further "skewed" generational distinctions amongst cross-cousins of one's matrilineage (Crow) or patrilineage (Omaha), while removing generational distinctions for other cross-cousins. *Sudanese* systems, on the whole, add a distinction between maternal- and paternal- cross- and parallel-cousins, and fully descriptive systems discriminate all eight kinds of cousins by gender and that of connecting relatives.

Moving from *Hawaiian* to *Sudanese*, we see an increase in paradigmatic complexity, as more terms are used to describe the same number of relations. This increase is structured in the sense that distinctions comprise an implicational hierarchy (see Fig. 1). This structured variation in cousin terminology is a general aspect of kinship typology. Kinship systems, like other cognitive category systems, are presumed to be inherited through observation, imitation, and instruction. They are subject to small variations in replication, and the success of the variants hinges on two crucial general aspects of cognition—the ease with which the system can be learned and its goodness-of-fit in modeling the outside world. We can call the former *learning pressure* (see Tomasello, 2009) and the latter external *social practice* (see Bybee & Hopper, 2001).

These pressures tie back to the issues raised in Section 1. A cognitive category system must be learned by the individual, so a combination of salient environmental input (how culture shapes cognition) and various cognitive biases (how cognition shapes culture) will compete in shaping it. The question is (a) what form these biases take and (b) how they map to more general aspects of the social environment.

1.2. Learning pressures, population size, and grammatical complexity

Learning pressure manifests both in the variability of input received by the learner and the learner's own cognitive biases. Input variability affects category learning on the sound and the word level (Maye & Weiss, 2003; Maye et al., 2002; Rácz et al., 2017). The robustness of category learning is increased if information is distributed across a larger number of contexts. For instance, hearing the same word from multiple speakers makes it

easier to recognize, process, and learn that word, although this claim has been called into question (see e.g., Atkinson et al., 2015). At the same time, adult second- language learners tend to process language differently from native child learners in that they select for variants of smaller morphological complexity (see e.g., DeKeyser, 2000; Hudson Kam & Newport, 2009). This means that context variability and the ratio of child and adult learners will have a long-term effect on linguistic complexity (for an alternate account, see Atkinson et al., 2018).

For a given language, both factors correlate with the number of speakers. What follows is that we expect a correlation between linguistic category complexity and the size of the speaker population. Nettle (2012) provides an excellent summary of the evidence on the correlation between population size and linguistic category complexity. He notes (p. 1829) that "[l]anguages of small communities tend to have smaller phonological inventories, longer words and greater morphological complexity than languages spoken in larger communities." That is, the morphology of "larger" languages tends to have less paradigmatic complexity.

Lupyan and Dale (2010) point to the role of adult learners in the correlation between population size and morphological complexity, arguing that a large ratio of adult learners results in morphologically simpler languages with more lexical marking. This is consonant with the overall picture, summarized by Nettle, that an increase in population size comes together with a decrease in morphological complexity. Bromham et al. (2015), using a sample of Polynesian languages, find that larger populations are more prone to gain new word forms in the basic vocabulary while smaller populations are more prone to lose forms within the same vocabulary. Reali et al. (2018) offer a formal modeling treatment of how a variant's ease to be learned affects its diffusion in the community, and how this correlates with the size and composition of the community. Sinnemäki and Di Garbo (2018) highlight that, in looking at group size and morphological complexity, the number of adult learners (L2 speakers) does not trivially correlate with population size and that the effect on morphological complexity varies across morphological domains.

Grammatical/morphological complexity in this literature typically refers to paradigmatic complexity, introduced in Section 1. In larger speaker groups, grammatical relations are less likely to be expressed by different forms of the same word (the word's paradigm) and more likely to be paraphrased by a sequence of words. English has about 340 million native speakers and two forms for each noun. Hungarian has about 13 million native speakers and about 16 forms for each noun. The Hungarian form "házában" (house-`Poss3sg-loc`) translates in English as "in his/her house." Here, English makes up for paradigmatic complexity with syntagmatic complexity.

While we are not aware of previous cross-cultural work on kinship complexity and group size, paradigmatic and syntagmatic complexity readily apply to kinship terms. Polish has the term "siostrzenica" to refer to a *sister's daughter* which can only be para-phrased in English (as "niece" does not specify the gender of the parent). Here, again, Polish shows higher paradigmatic complexity, compensated by higher syntagmatic complexity in English.

Larger populations with a large amount of adult learners and high variability should have kinship systems with lower paradigmatic complexity, using fewer words to describe the same relations. We find support for this when we look at the use of kinship terms and

related linguistic practices in specific small communities. For example, in Murrinhpatha in Northern Australia (Blythe, 2013) and in Datooga in Northern Tanzania (Mitchell, 2016), learning kinship terms or kinship-related practices, such as name avoidance, requires a great extent of familiarity with the kinship relations of the entire local community. Farber (1975) discusses, on a greater scale, how this type of familiarity changes in larger communities with shifts in kinship practice.

Previous research has suggested a number of ways in which population size can influence paradigmatic complexity in language. This includes the ratio of adult learners, input variability, and ease of transmission in the community, all of which are correlated with the size of the overall speaker population. All these arguments can apply to the paradigmatic complexity of kinship systems. The essential point here is that a set of learning biases can mediate the effects of population size, and, as a result, become mainly responsible for variation in kinship systems.

1.3. Social practice

An alternative explanation for the paradigmatic complexity of kinship systems is that these are shaped by the specific social practices that make use of kinship terms; patterns of wealth transfer, marriage, or inheritance. Links between kinship systems and such practices have been extensively documented in the cultural anthropology literature (see for example the Explaining Human Culture database of hypotheses at the Human Relations Area Files & Inc, 22017), based on correlations in the Ethnographic Atlas (Murdock, 1967), the Standard Cross-Cultural Sample (Murdock & White, 1969), or specific language groups. We provide here some examples to give a flavor of the kinds of associations described in the literature, but these are by no means exhaustive.

Murdock (1947) finds a correlation between the use of *Crow* and *Omaha* systems (which discriminate cross- and parallel-cousins on the father's or the mother's side, respectively), *exogamy* (marrying outside the community), and/or unilinear descent (traced on the mother's or the father's side). Here, the social pressure comes from distinguishing who is and who is not in one's matrilineage or patrilineage. Murdock (1949) returns to these findings and adds that a *clan* system or exogamous moieties also favor *Crow/Omaha* cousin terms. In both these instances, the kinship systems reflect who may be available for marriage. Coult (1965) finds correlations between, on the one hand, *Omaha* cousin terms, *patrilineal descent*, and preferential *matrilineal cross-cousin marriage* and, on the other hand, *Crow* terms, *matrilineal descent*, and preferential *patrilineal cross-cousin marriage*. *Iroquois* terms (cross- and parallel-cousins are discriminated on both parent's side) correlate with preferential *bilateral cross-cousin marriage* in his sample. We should note that more recent work, relying on more advanced methods, puts at least some of these claims to question, as in the case of Guillon and Mace (2016), whose comparative phylogenetic analysis finds little evidence for the co-evolution of cousin terms and descent organization in Bantu languages.

Goody (1970) surveys cousin terms and finds a correlation between *Hawaiian* terms and the prohibition of cross-cousin marriage. A cross-cousin will be called "sibling" in a

Hawaiian system, so here the semantic system reflects the incest taboo. *Iroquois* terms are found with preference for cross-cousin marriage, and it is precisely some cross-cousins who might be outside one's lineage and thus available for marriage. Much like Coult, Goody finds a correlation between *Omaha*, *Crow*, and *Eskimo* terms and *patrilineal*, *matrilineal*, and *bilateral* descent, respectively. Köbben et al. (1974) support Goody's findings on the link between *Hawaiian* terms and the prohibition of cross-cousin marriage, and establishes a correlation between *Crow/Omaha* terms and prohibition of marriage into the line of cross cousins.

The intuition underlying these correlations is that the semantic system reflects social practice. If marriage is permitted to certain types of siblings/cousins, these types should be named separately; emphasis on one line of descent should make distinctions on that line more salient.

1.4. Hypotheses

The broader cognitive literature on category complexity and population size and the anthropology literature on kinship terms and social practice provide us with two hypotheses that are testable against a cross-cultural sample.

1. **The main source of kinship complexity is speaker group size.** Kinship systems vary in paradigmatic complexity. Paradigmatic complexity decreases with an increase in population size. This means that larger or more complex communities will use simpler kinship systems, irrespective of Sprachbund and language family effects.
2. **The main source of kinship complexity is associated social practice.** Kinship systems vary in structure. Various cultural practices (such as marriage or inheritance) rely on kinship distinctions. This means that the use of a kinship system will be linked to the presence or absence of these practices across communities: A society with prevalent cousin marriage or a society with asymmetrical patterns of descent and transfer will make more distinctions across siblings and cousins.

2. Methods

We examine the distribution of cousin term systems across 1,291 societies in the D-PLACE online ethnographic database (d-place.org) (Kirby et al., 2016), largely based on data from the Ethnographic Atlas (Murdock, 1967).[1] We work with 936 societies which have available information on kinship systems. The distribution of kinship systems can be seen in Fig. 2. Here, we display the variation in a subset of societies (those from the 12 largest language families represented in D-PLACE) to visualize the influence of shared linguistic history on kinship diversity.

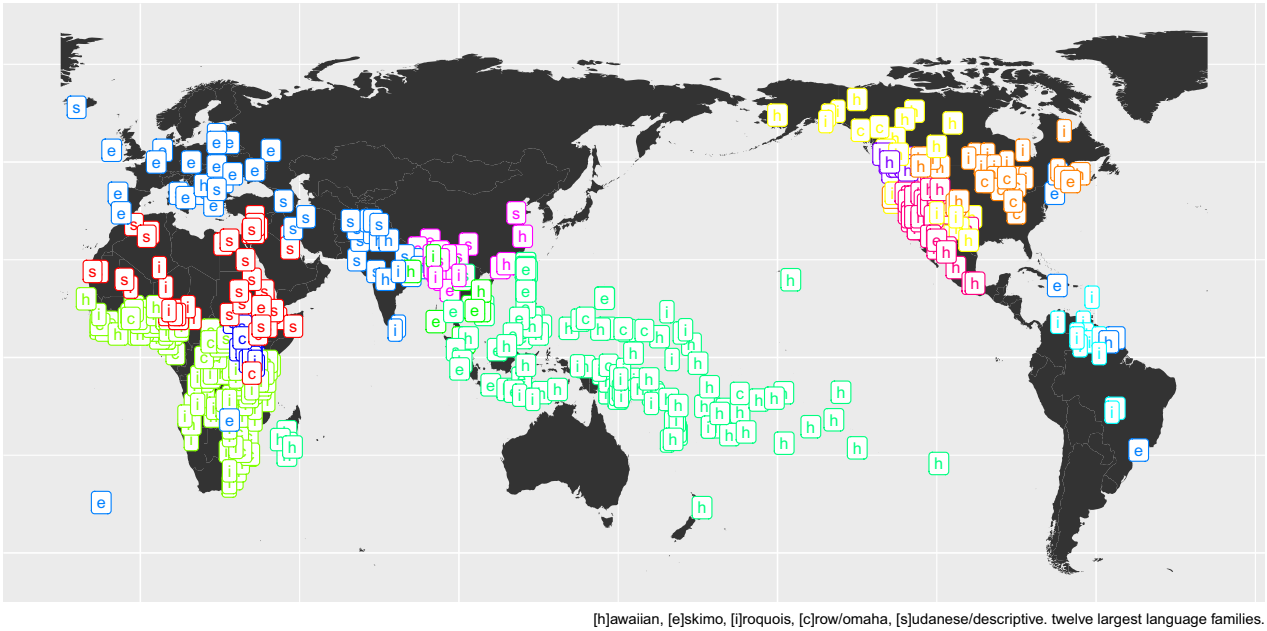


Fig. 2. Global distribution of kinship systems across twelve largest language families in D-PLACE ([H]awaiian, [E]skimo, [I]roquois, [C]row/Omaha, [S]udanese/Descriptive)

2.1. Outcome

Our outcome variable is the complexity of the kinship system which we quantify based on the number of distinctions across cousin terms, as discussed in Section 1.1 (EA027 in the Ethnographic Atlas—for details, see Appendix). We posit the ranking of *Hawaiian* < *Eskimo* < *Iroquois* < *Crow/Omaha* < *Sudanese/Descriptive* (see Fig. 1).

This quantification is simplified. For example, many *Hawaiian* systems make a distinction between Ego's younger and older siblings/cousins. At the same time, the lack of distinction persists between "sibling" and "cousin" in these systems, such that our ranking still holds.

More complex characterizations of kinship system complexity, such as a calculation of entropy, require systematic kinship term lexical data comparison. We are currently building such a dataset to be publicly available (KinBank, see https://excd.org/research-activities/varikin), but in order to make large global comparisons here we focus on cousin terms.

2.2. Population-level factors

We have two groups of population-level factors.

Hypothesis 1 hinges on *population size* (EA202) and *community size* (EA031), represented in the Ethnographic Atlas data in D-PLACE. Population size is defined therein as the size of the ethnic group as a whole. Community size represents an average population of local communities and is equally important as it determines the amount of variation and adult/child learner ratios in the individual learner's language environment.

However, a large amount of data is missing for population size (27.03%) and community size (46.26%). Other indicators of community size are available: *settlement patterns* (EA030), *the number of jurisdictional levels in the local community* (EA032), *the number of jurisdictional levels beyond the local community* (EA033). The first one captures settlement size and complexity, categorizing societies from migratory bands to complex permanent settlements (pairwise correlation with population size (logged): $r = 0.41$). The second one focuses on the power hierarchy within settlements, ranging from independent families to clan districts ($r = 0.22$). The third one pulls focus onto inter-settlement patterns, ranging from no authority beyond the local community to chiefdoms to complex states ($r = 0.58$). While *subsistence* (EA042) is not a direct proxy of population size, different subsistence types will typically support populations of various sizes: Forager populations are generally smaller, and societies that rely on intensive agriculture can be larger ($r = 0.44$, using numeric subsistence complexity). Following Botero et al. (2014), we combine these factors with population size and community size to estimate social group size and social complexity.

Hypothesis 2 hinges on a set of cultural practices coded in the Ethnographic Atlas data in D-PLACE. These are the *prevalence of cousin marriage* (EA023, ranging from complete proscription to the allowance of marriage to first cousins), *community marriage patterns* (EA015, exogamous, endogamous, or agamous), and *descent* (EA043, patrilineal, matrilineal, bilateral, ambilineal, or mixed); see the Appendix for details.

2.3. Grouping factors

It is evident from Fig. 2 that the kinship system of a community is highly correlated with the language spoken in the community and the community's location. For example, groups across the Pacific in the large Austronesian language family mostly have *Hawaiian* kinship. European languages mostly have *Eskimo* kinship, including Hungarian, a non-Indo-European language. As a consequence, we incorporate language family and geographical proximity in the analysis by adding a grouping factor for language family and one for the named geographic region, both taken from D-PLACE.

2.4. Data analysis

The dataset is challenging in two ways, both typical for cross-cultural data. Predictor variables are correlated (e.g., a society with unilineal descent is more likely to permit cousin marriage) and a lot of data are missing—*population size* and *community size* are two good examples. Our approach aims to account for these issues without the use of stepwise regression modeling, which increases the likelihood of Type I errors (Flom & Cassell, 2007).

We use a multilevel ordered categorical model to fit on the data (Wood, 2006; Wood et al., 2016) in R (R Core Team, 2016). We use ggplot to create the plots (Wickham, 2009). Our outcome variable is the type of kinship system, ranked by complexity (*Hawaiian* < *Eskimo* < *Iroquois* < *Crow/Omaha* < *Sudanese/Descriptive*). An ordered categorical

model estimates an intercept for all levels of the outcome variable and assumes that they have a set order.

We fit two hypothesis-testing models, one using predictors relevant to Hypothesis 1 (*population size (logged)*, *community size*, *jurisdiction*, *local jurisdiction*, *settlement patterns*, and *subsistence*) and the other using predictors relevant to Hypothesis 2 (*prevalence of cousin marriage*, *descent*, *community marriage practice*). We do not impute missing data and instead fit each model on the maximum number of societies with available data for all predictors. This leaves us with $n = 366$ for *Model 1* and $n = 779$ for *Model 2*). We then remove predictors with $-1.5 < z < 1.5$ and use a chi-square test on the difference in scores and degrees of freedom as well as the Akaike Information Criterion for model selection. Subsequently, streamlined models are refit on the maximum number of data available. This procedure is followed to arrive at a best fit for each model.

The predictors from the best fits of the two models—*local jurisdiction*, *subsistence*, *descent*, and *cousin marriage*—are combined in *Model 3*. These are predictors that are relevant to testing our hypotheses. We also have evidence of their robustness. Using all possibly relevant predictors would inflate multicollinearity and create a data imputation problem, both of which are largely avoided using our approach.

This model is fit on all societies with data available on all these predictors ($n = 743$). To check robustness, *Model 3* is also refit on data subsets (a) excluding Indo–European societies, (b) excluding the largest 5% of societies, and (c) limiting the dataset to societies in the standard cross-cultural sample (SCCS; Murdock & White, 1969), albeit using the same predictors derived from the Ethnographic Atlas.

Our justification for (3a) is that many Indo-European speakers are members of Western, rich, industrialized democracies and these groups tend to be outliers of broader ethnographic variation (Henrich et al., 2010). We have a similar reasoning for (3b)—we use population size to exclude the largest 5% and while population size data are missing for many societies, we expect that, for large societies, it will be more readily available, allowing for our method of exclusion. We use (3c) to render testing more robust, because the SCCS is a widely used sample of human societies that is deliberately stratified by region to minimize the effect of ancestry and diffusion ("Galton's Problem" and spatial autocorrelation), and the sample was chosen to be representative of human lifeways.

Finally, to explore these relationships at finer resolution than the global level, we take a phylogenetic approach (Blute & Jordan, 2018; Mace & Pagel, 1994). We use language phylogenies (evolutionary trees) of three large representative language families, and a subset of the cultural data used for our models to calculate the phylogenetic signal for a set of traits. By mapping cultural data onto the tips of a language tree, we are able to measure how well a trait is structured by the branching relationships of cultural history. If a trait is primarily vertically inherited from parent to offspring cultural groups, then phylogenetic signal will be high. If traits are subject to cultural borrowing, independent innovation, stochastic change, or rapid contextual change, signal will be low.

3. Results

We quote four models here and discuss one in detail (see Table 1; note that we use zero-based numbering. We return to robustness checks and high resolution phylogenetic analysis in Section 3.2.

Model 0 has no population-level effects and only contains grouping factors for *language family* and *geographic region*. As we can see, this model already explains some amount of variation (18%), underscoring that *language* family (shared history) and *region* (spatial diffusion opportunities and shared adaptation) are very important factors in determining the kinship system used in a community. These grouping factors are present in all subsequent models.

Model 1 is fit to determine the relevance of predictors for Hypothesis 1 (i.e., social relevant are *jurisdiction on a local level* and *main mode of subsistence*. *Population* and *community size*, *jurisdiction beyond the local level* and *settlement patterns* are not relevant in predicting kinship system. This can be either because these factors are not directly relevant to kinship complexity, or because too many data are missing for meaningful inference.

Model 2 is fit to determine the relevance of predictors for Hypothesis 2 (social practice affects kinship complexity). The fixed effects that remain relevant are *descent* and *prevalence of cousin marriage*. *Community marriage patterns* are not relevant in predicting the use of a particular kinship system.

The relevant aspects of models 1 and 2 are that both explain some amount of variation in the data, but that the additional explaining power of Model 1 is relatively low—social complexity plays little, if any role.

Model 3 is our combined model. It contains the relevant predictors from *Model 1* and *Model 2*. The summary of the fixed effects can be seen in Table 2. The base levels are "intensive agriculture" for subsistence and "patrilineal" for descent. These are essentially arbitrary, though the plurality of societies are patrilineal.

Our proxy of community size, *local jurisdictional hierarchy*, is not a robust predictor of kinship complexity. Robust predictors ($-1.5 > z > 1.5$) are *subsistence*, *prevalence of cousin marriage*, and *descent*. *Pastoralist* societies are more likely to have more complex kinship systems. We had no starting assumptions about pastoralists, so this is a curious result and we return to it in the discussion. Kinship complexity increases with more prevalent cousin marriage. *Symmetrical* descent systems (such as *bilateral* or *ambilineal*

Table 1
Summary statistics for models

Model	No. Observations	Cumulative Deviance Explained
0 (only grouping factors)	936	0.18
1 (social complexity)	807	0.19
2 (social practice)	841	0.23
3 (combined)	743	0.23

Table 2
Summary of the fixed effects, Model 3 (Predictor name, estimated effect, standard error, and *z*-value)

	Estimate	*SE*	*z*-value
(Intercept)	−0.073	0.511	−0.142
local jurisdictional hierarchy	−0.005	0.137	−0.036
subsistence:extensive agriculture	0.062	0.217	0.285
subsistence:foraging	−0.149	0.276	−0.540
subsistence:pastoralism	0.882	0.382	2.310
cousin marriage	0.461	0.078	5.904
descent:matrilineal	−0.115	0.243	−0.473
descent:bilateral or quasi-lineage	−1.656	0.232	−7.146
descent:duo- or ambilineal	−1.100	0.301	−3.656
descent:mixed	−1.456	0.384	−3.789

ones) are likely to have less complex kinship systems than *unilineal* (*patri-* or *matrilineal*) ones.

While model fitting is explicitly designed to avoid multicollinearity, it remains an issue given the nature of the predictors. A *post hoc* inspection of variance inflation factors (Clifford, 2016) reveals that confidence intervals for the robust predictors can be inflated up to a rate of 2.1–3.01 times. This especially casts a doubt on the effect of *pastoralism*, which is estimated to be relatively small in the first place. The other predictor estimates are larger and more resilient in the face of possible multicollinearity effects.

Fig. 3 illustrates the global distribution of some of the relevant predictors—descent type, cousin marriage, and subsistence—against kinship system type. It demonstrates the spatial (and historical) clustering of many co-associations in the ethnographic data. For example, across Northern Africa and the Middle East, we see substantial co-occurrence of pastoralism, Sudanese/Descriptive kinship systems, and marriage with first cousins. These co-occurrences are not new observations, and have been attributed as adaptations to unproductive environments in the case of pastoralism (see Pryor, 2005), and in the case of Sudanese kinship, as logical-linguistic indicators that some relatives are marriageable while others are not. Importantly, our results show that while shared history and environment can account for some co-occurrence in language and culture between societies, there is further variation left to explain.

3.1. Predictions

Fig. 4 shows the predictions of *Model 3*, aggregated across levels of the predictors, with aggregated estimated standard errors. The model gives a probability for society having each kinship system; these add up to 1. Fig. 4 aggregates the predicted probabilities and standard errors across levels of the predictors.

For instance, (upper left panel) the likelihood of having a simpler Hawaiian system drops with the increase in the prevalence of cousin marriage. In contrast, the likelihood of having a more complex Sudanese system increases under this condition. One has to

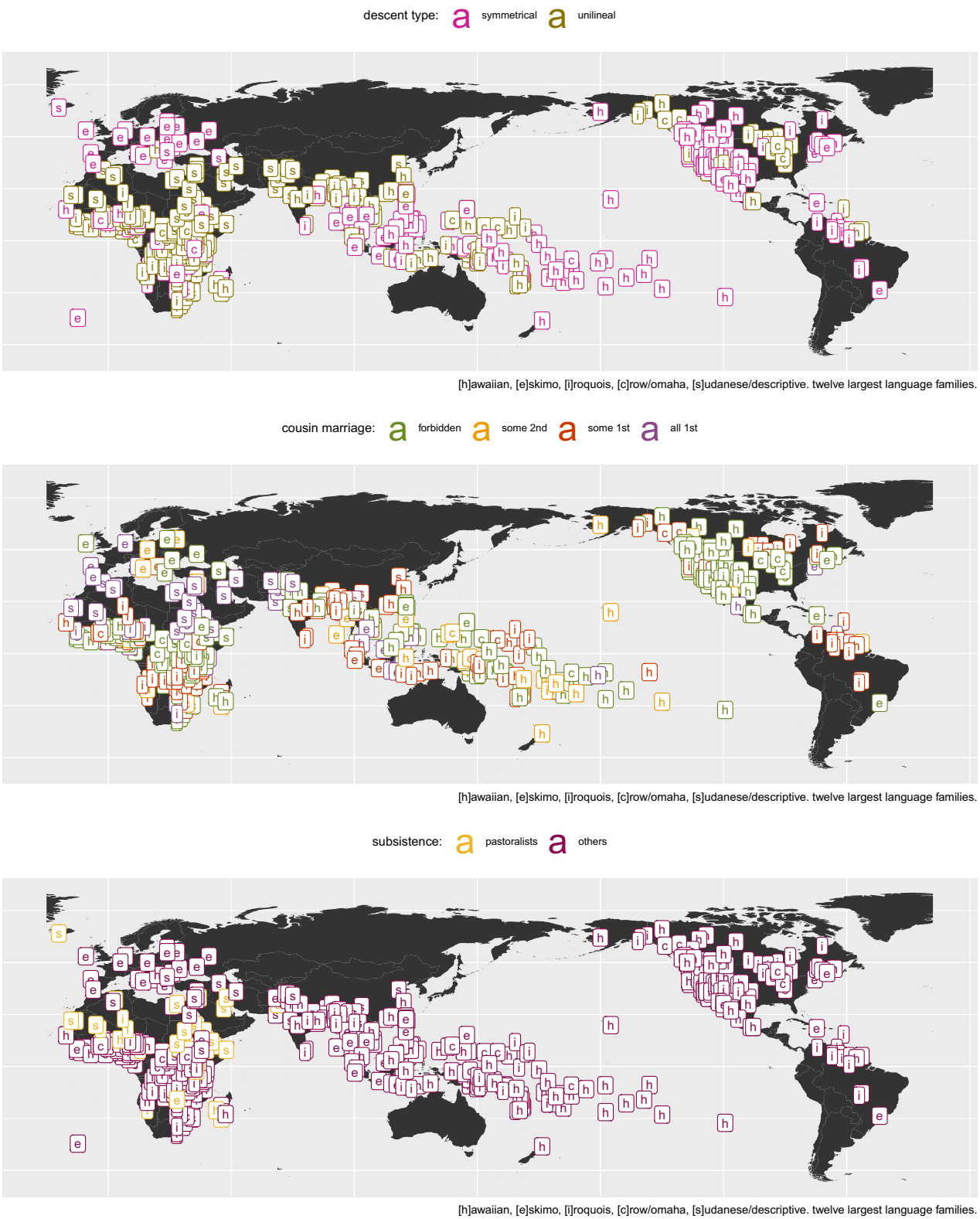


Fig. 3. The distribution of social predictors and kinship systems. Panel (a) shows kinship system versus descent category. Symmetrical descent includes societies coded as bilateral or double descent; unilineal includes societies coded as patrilineal or matrilineal. Panel (b) shows cousin marriage practice: forbidden, some 2nd cousins, some 1st cousins, all 1st cousins. Panel (c) divides societies by whether they are pastoralists or not

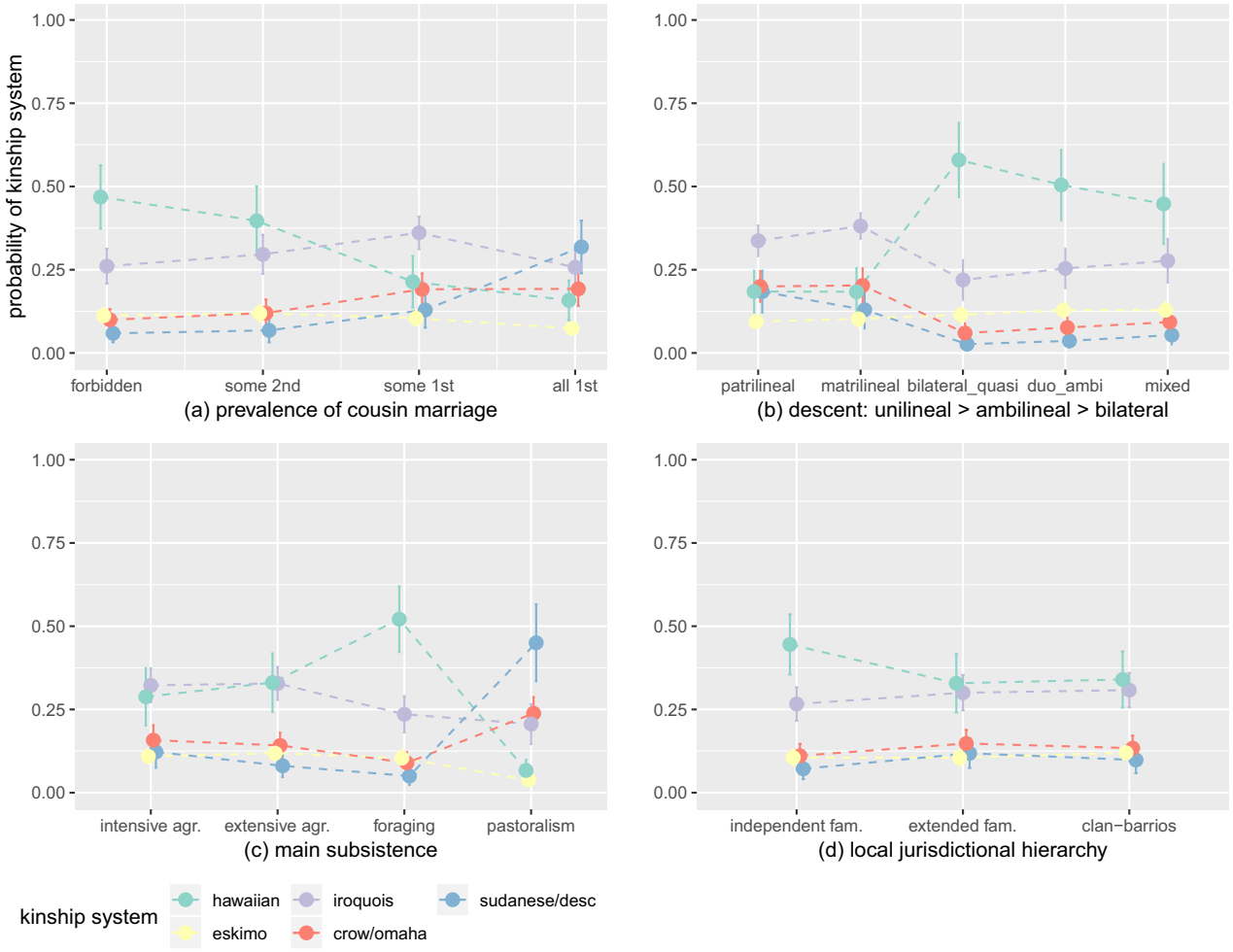


Fig. 4. Predictions of the combined model. The ordered outcome categories are *Hawaiian* < *Eskimo* < *Iroquois* < *Crow/Omaha* < *Sudanese/Descriptive*. For each panel, we show the probability of any particular kinship system for a given category of (a) cousin marriage (b) main form of subsistence (c) descent system and (d) local jurisdictional hierarchy. (a) Cousin marriage is categorized as (i) all forms forbidden, (ii) some 2nd cousins, (iii) some 1st cousins, (iv) all 1st cousins; (b) subsistence is categorized as (i) intensive and (ii) extensive agriculture, (iii) foraging, and (iv) pastoralism; (c) descent systems are categorized as unilineal/ambilineal/bilateral, and, specifically, as (i) patrilineal, (ii) matrilineal, (iii) bilateral, (iv) ambilineal, (v) mixed; (d) local jurisdictional hierarchy is categorized as (i) independent and (ii) extended families, (iii) clan-barrios.

bear in mind that the model assumes these systems to be ordered according to complexity.

This means that the subsistence effect is more robust for pastoralists (upper right panel) than for foragers. This is because, in the former case, we see, for example, both a drop in the likelihood of Hawaiian and an increase in the likelihood of Sudanese. Kinship complexity is higher for unilineal than for symmetrical systems, driven by all types except Crow/Omaha and Eskimo (lower left), while, despite the drop in the likelihood of Hawaiian, local political complexity overall does not covary with kinship complexity in this model (lower right).

3.2. Robustness checks and phylogenetic signal

Fitting *Model 3* on data (a) after excluding Indo–European-speaking societies or (b) the largest 5% in terms of population size yields very similar results, except that, in the latter case, the distinction between *pastoralists* and other subsistence types is diminished.

In terms of (c) comparing the Standard Cross-Cultural Sample and the Ethnographic Atlas: All 186 societies of the SCCS are present in the Ethnographic Atlas, but only 161 have all the required data, so we fit the model on these societies. This yields similar results on the population-level predictors: Pastoralists and more prevalent cousin marriage practices are correlated with more complex kinship systems, along with unilineal (as opposed to symmetrical) descent systems. One main difference is that language family and region are no longer significant predictors in this model, which is to be expected given the stratified purpose of the SCCS.

On the whole, our regression analysis finds strong effects of *cousin marriage* and *descent*, along with an effect of *subsistence* (pastoralists/other main sources of subsistence) on the complexity of the kinship system in the societies of the sample. The effects remain robust if we take into consideration the skewing effect of Indo-European or very large societies, and also remain for the smaller set of societies in the SCCS. However, one simplification of the regression model is that it treats language families as trees with no internal structure, effectively assuming the same distance between all languages that belong to a given family.

In order to test for cultural inheritance using a higher resolution, we use phylogenetic "D" tests to determine if kinship systems display phylogenetic structure (Fritz & Purvis, 2010). A "D" test provides a value to express the extent to which patterns are constrained by the evolutionary relationships between societies (cultural history) or dispersed randomly across the phylogenetic tree. We use language family trees (phylogenies) from D-PLACE to estimate the D statistic and its associated p-values for the most common kinship system types in three different language families: Austronesian (85 observations), Bantu (69 observations), and Uto-Aztecan (22 observations). Because multiple histories might be inferred from any linguistic data set, for each family we test D across 1,000 trees derived using Bayesian phylogenetic inference (Dunn et al., 2011; Gray et al., 2009; Grollemund et al., 2015). Each of these trees represents a slightly different but highly plausible reconstruction of cultural history. We infer a value of D for kinship system types that are seen in more than 10% of societies on the language tree: Eskimo, Hawaiian, and Iroquois systems in Austronesian; Hawaiian, Iroquois, and Omaha systems in Bantu; and Crow, Eskimo, Hawaiian, and Iroquois systems in Uto-Aztecan.

Across all three families we find that around half of the kinship systems show meaningful phylogenetic signal (i.e., D close to or less than 0) at a fine-grained local level, demonstrating the importance of shared ancestry in structuring complexity in semantic systems even in closely related languages. The D values can be seen in Table 3.

Table 3
D-statistic tests of phylogenetic structuring for terminological types, in three large language families

		Present	D-Statistic
Austronesian (n = 85)	Eskimo	14	−0.498
	Hawaiian	48	0.659
	Iroquois	15	0.095
Bantu (n = 69)	Hawaiian	9	0.402
	Iroquois	44	0.162
	Omaha	8	0.780
Uto-Aztecan (n = 22)	Hawaiian	16	−0.596
	Iroquois	4	−2.336

A D-statistic close to or greater than 1 indicates a random distribution, not structured by the phylogeny. A D statistic close to 0 implies consistency with Brownian motion along the branches of the phylogeny, that is, structuring by descent. D less than 0 implies strong phylogenetic clustering.

4. Discussion

We used multilevel ordered categorical models to account for an axis of kinship system complexity across hundreds of human societies. We tested two hypotheses that emerged from the literature on the correlates of semantic complexity and kinship systems: the effects of speaker group size and cultural practices. Our analysis of the evidence does not support a link between an increase in community size and a decrease in kinship system complexity, but we do find support for the position that kinship systems are co-determined by specific practices of marriage and descent. In doing so, we also assessed the extent to which spatial proximity and shared ancestry influence our measure of kinship complexity. We found that while both explain some variation at a global scale on a large unstratified data set, detecting these effects is subject to the scale and type of analysis.

Our evidence for both main findings remains robust when we control for the effect of language family and spatial proximity is resilient to multicollinearity, and our analyses do not hinge on the inclusion of data points from large-population states or Indo-European societies. This is striking, as large cross-cultural analyses are inevitably plagued by noise in the data, related to the inherent patchiness and unstructured nature of much ethnographic data. Data on population and community size are difficult to extrapolate from ethnographic sources where a formal census is not available, and they are restricted to a particular time and place foci (Ember et al., 1992). Despite these complexities, our aim was to avoid the methodological pitfalls related to the regression analysis of large sets of covarying factors in incomplete data, such as the use of unprincipled top–down stepwise regression (Flom & Cassell, 2007). Instead, we opted to rely on expert judgment (Galison & Daston, 2007) in choosing a set of factors to compare two plausible hypotheses, adapted to variation in kinship systems, and to see which one explained more variation in our data.

The low predictive power of our models strongly suggests that kinship systems evolve in complex, multifaceted processes which are difficult to capture in a correlational study. While other studies have detected some broad predictive trends in cultural features, such as an association between poorer environment and the presence of a belief in moralizing high gods (Botero et al., 2014), it may be that here the global scope of our analyses masks important regional cultural dynamics of kinship systems. Our tests for phylogenetic signal support this supposition: Different kinship systems show phylogenetic clustering in different language families, echoing the lineage-specificity found in word-order studies (Dunn et al., 2011). Ultimately, language family remains the most important predictor of kinship system in our analyses. Given that some large language families such as Indo-European, Austronesian, and Bantu are associated with Neolithic spread of agricultural technologies (Bellwood, 2005), and that changes in subsistence have been considered to be catalysts for change in social organization (Apostolou, 2010; Ember et al., 1992; Nimkoff, 1965; Walker et al., 2013), we suggest that language–family-level approaches using comparative phylogenetic methods (Jordan, 2013) may test these coevolutionary hypotheses in future.

While our results suggest that our measure of kinship complexity is determined by specific practices and not by community size or population size, the effect of *subsistence* on kinship complexity remains an exception. Pastoralists tend to have more complex kinship systems than agriculturalists or foragers. Holden and Mace (2003) discuss the relationship between the emergence of *patriliny* and cattle ownership in the Bantu. They explain the apparent connection (cattle ownership leads to patriliny) in terms of wealth transfer—herds of cattle need to be held together to defend and inherit, favoring male heirs. This explanation, scaled upwards, could apply to our data. Cattle ownership shapes wealth transfer practices and these, in turn, shape kinship. This means that subsistence should be interpreted as a proxy for social practices rather than a proxy for overall complexity of social organization. Our result on pastoralism should be treated with reservations, however, as it is relatively weak and more sensitive to predictor multicollinearity.

The covariation of kinship systems with specific practices, rather than group size, has implications for the debate on the relationship between linguistic and speaker group complexity. Works such as Nettle (2012) and Reali et al. (2018) point to and formalize broad biases in learning and transmission for aspects of language that covary with group size. These include low-level, closed sets of function words, like morphology, and higher-evel, open sets of content words, like vocabulary.

Kinship systems are closed sets of content words, entwined with social practice. In some cases, kinship is able to "invade" the grammar and be marked on, for example, verb agreement (Blythe, 2013). This means that it is an ideal testing ground for hypotheses on the effects of broad biases and specific practices on language use. Our phylogenetic signal analyses are suggestive: On our measure of complexity, the most complex systems that we tested (Crow, Omaha) are not structured by long-term shared ancestry and perhaps more liable to change from learning pressures. What we infer from cross-cultural variation in kinship is that caution is warranted in attributing patterns of cross-cultural

variation to broad biases because these patterns are more likely to be mediated by specific cultural practices. No doubt, these practices are sensitive to group size (exemplified by the difference between pastoralists and other forms of subsistence in Bantu language groups). It is simply to say that a rounded account of explaining cognitive diversity should consider macro (cultural evolutionary) as well as micro (cognition and learning) drivers. Given that kinship is a good example of an intermediate lexical class, these results could be generalized as informative for the broader debate.

The intermediate nature of kinship systems in language invokes the parallel of a separate debate in anthropology and archaeology on the correlation between population size and *toolkit size* (Aoki, 2018; Henrich, 2004). The major difference is that unlike tools, cultural practices or the specialized vocabulary that goes with them (e.g., kinship words) —*and* the systems in which they articulate—must be learned by everyone in the community. As a consequence, many of the explanations proposed for the correlation between toolkit size and population size may not be applicable to kinship.

This paper builds on the existing literature on language complexity in general and kinship systems in particular. It is novel in extending arguments on population size and complexity to kinship system and comparing population size and social practice at an unprecedented scale. The results presented here are both larger in scope and more statistically principled than previous work on the correlates of kinship systems, rendering our findings fairly robust. Further, we see our contribution as demonstrating how kinship categories, a key aspect of social cognition, can be approached in a comparative and cultural-evolutionary manner alongside the standard individual-level experimental and modeling tools of cognitive science. Further research combining the macro and the micro can help give a well-rounded account of the constraints on human social categories.

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Note

1. Code and data available at http://doi.org/10.5281/zenodo.2625861.

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Appendix: Coding of Ethnographic Atlas variables

For details, see https://github.com/petyaracz/RaczPassmoreJordan2018.

EA Variable	Name	EA Code: Coding Used in Paper	Type in Paper
EA015	Marriage types	1,2: endogamous; 3: agamous; 4,5,6: exogamous	Factor
EA023	Cousin marriage	7,8: 1; 11,12: 2; 1,2,3,4,5,6,9,13: 3; 10, 4	Ordered
EA027	Cousin type	4: hawaiian; 3: eskimo; 5: iroquois; 1,6: crow/omaha; 7,2: sudanese/descriptive	Ordered
EA031	Community size		Ordered
EA030	Settlement patterns		Ordered
EA032	Local jurisdiction		Ordered
EA033	Jurisdiction		Ordered
EA042	Subsistence	7: intensive agriculture; 5,6,9: extensive agriculture; 4: pastoralism; 1,2,3: foraging	Factor

(continued)

Table . (continued)

EA Variable	Name	EA Code: Coding Used in Paper	Type in Paper
EA043	Descent type	1: patrilineal; 6,4: bilateral/quasi-lineages; 3: matrilineal, 2,5: duolateral/ambilineal; 7: mixed	Factor
EA202	Population size		Numeric

APPENDIX G

Appendix G: Text analysis shows conceptual overlap as well as domain-specific differences in Christian and secular worldviews

My contribution to this paper was to conceptualise the study, design the methodology, curate the data, perform the analysis, and to aid in writing and reviewing the manuscript.

This paper deviates from the kinship themes of this thesis, but continues the aim of maximizing the amount of variation analysed. The goal of this paper was to determine whether people from Christian and non-religious backgrounds understand the world in similar or different ways by analysing free-text answers and using natural language processing. By producing a method that analyzes free-text answers, we no longer need to restrict the study of between-group differences to Likert scale analysis, but can allow participants to express themselves freely. Here, new methods and technology allow us to broaden the variation that participants produce, and that we can analyse, to give us a more specific view of how different people and groups perceive the world.

The result of this paper found that Christian and non-religious people's explanations vary depending on the kind of phenomena being explained. Non-religious people provided more similar explanations for natural than supernatural phenomena, whereas Christian explanations were relatively similar across both natural and supernatural phenomena. This challenges the idea that religious systems standardize and restrict people's worldviews in general, and instead suggest this effect is domain specific.

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Brief article

Text analysis shows conceptual overlap as well as domain-specific differences in Christian and secular worldviews

Joseph Watts[a,d,e,f,*], Sam Passmore[b], Joshua Conrad Jackson[c], Christoph Rzymski[d], Robin I.M. Dunbar[e]

[a] Religion Programme, University of Otago, Dunedin 9054, New Zealand.
[b] Department of Anthropology & Archaeology, University of Bristol, UK
[c] Department of Psychology and Neuroscience, University of North Carolina at Chapel Hill, United States of America
[d] Department of Linguistic and Cultural Evolution, Max Planck Institute for the Science of Human History, 07745 Jena, Germany
[e] Department of Experimental Psychology, University of Oxford, Anna Watts Building, Oxford OX2 6GG, UK.
[f] Center for Research on Evolution, Belief, and Behaviour, University of Otago, Dunedin, New Zealand.

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ABSTRACT

Theories differ over whether religious and secular worldviews are in competition or represent overlapping and compatible frameworks. Here we test these theories by examining homogeneity and overlap in Christian and non-religious people's explanations of the world. Christian and non-religious participants produced free text explanations of 54 natural and supernatural phenomena. Using a new text analytic approach, we quantitatively measure the similarity between 7613 participant generated explanations. We find that the relative homogeneity of Christian and non-religious people's explanations vary depending on the kind of phenomena being explained. Non-religious people provided more similar explanations for natural than supernatural phenomena, whereas Christian explanations were relatively similar across both natural and supernatural phenomena. This challenges the idea that religious systems standardize and restrict people's worldviews in general, and instead suggest this effect is domain specific. We also find Christian and non-religious participants used largely overlapping concepts to explain natural and supernatural phenomena. This suggests that religious systems supplement rather than compete with secular based worldviews, and demonstrates how text analytics can help understand the structure of group differences.

1. Introduction

People disagree over what happens when we die, whether we are alone in the universe, and the origins of life on earth. Religions are popularly seen as a major source of this disagreement, but it is not clear exactly how religions affect people's explanations of the world. Do religions force people to use a specific set of ideological concepts to explain the world? Or do religions simply add an additional layer of explanation?

One popular claim is that religions represent systems of concepts, termed "memeplexes," that replicate at the expense of alternative religious and secular worldviews (Dawkins, 2006; Dennett, 2006). These competition-based accounts predict that the worldviews of people with the same religious affiliation share more concepts than people with different religious affiliations. They also predict that religious systems homogenize adherents' worldviews by prescribing a divinely sanctioned doctrine. In support of competition-based accounts, studies show that priming religious explanations leads people to rely less on scientific explanations (Preston & Epley, 2009) and human agency (Dijksterhuis, Preston, Wegner, & Aarts, 2008).

Alternative theories argue that religious and secular worldviews explain different aspects of the world, and can be combined into a coherent conceptual system (Astuti & Harris, 2008; Gould, 1999; Subbotsky, 2001; Watts, 1997). These synthesis-based accounts predict that religious worldviews include the same kinds of concepts as secular worldviews, with the addition of an expanded set of supernatural concepts. In support of these accounts, research shows that religious individuals simultaneously endorse both natural and supernatural explanations of the same phenomena (Busch, Watson-Jones, & Legare, 2017; Cornelius, Lacy, & Woolley, 2011; Legare, Evans, Rosengren, & Harris, 2012).

Existing empirical studies analyzing the relationship between

* Corresponding author at: School of Social Sciences, University of Otago, Dunedin 9054, New Zealand.
E-mail address: me@josephwatts.org (J. Watts).

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natural and supernatural explanations have used Likert-scale responses, experimenter coded binary and categorical classification systems, or reaction times in binary evaluations (Busch et al., 2017; Kelemen, Rottman, & Seston, 2013; Legare et al., 2012; Nancekivell & Friedman, 2017; Preston & Epley, 2009; Woolley & Cornelius, 2017). These studies have provided important theoretical insights into the cognitive processes underlying supernatural beliefs, but their methodological approaches restrict the amount of information analyzed because they do not represent the extent of semantic overlap in people's explanations. These studies have also focused on how people explain specific kinds of phenomena, such as the causes of illness (Busch et al., 2017; Legare et al., 2012; Preston & Epley, 2009), or the reasons for unexpected, impossible or unlikely events (Cornelius et al., 2011; Nancekivell & Friedman, 2017; Woolley & Cornelius, 2017). One reason that both competition-based and synthesis-based accounts have found empirical support could be that religious people may synthesize science and religious based concepts for some kinds of phenomena, such as the causes of death, but treat religious and scientific concepts as competing for other kinds of phenomena, such as what happens after death.

Here we develop a new way of testing between competition-based and synthesis-based accounts across a variety of domains using text analysis. Text analytic methods can efficiently and systematically quantify the similarity between Christian and non-religious participants' explanations of a diverse range of phenomena. These data allow us to identify whether religious affiliations divide the kinds of concepts that people use to explain the world, and whether religious people use more homogeneous explanations than non-religious people.

2. Methods

2.1. Participants

A total of 245 participants were recruited for this study, but 33 were excluded due to low effort responses or inconsistencies between their pre-screened identity and the post-study questionnaire. For example, we excluded a participant that identified as “Wiccan” in the post-study questionnaire (a full description of exclusions is provided in the Supplementary Materials). After exclusions, our study included 212 participants from the United States of America, 101 who identified as Christians (55 female and 46 male), and 111 who identified as non-religious (51 female and 60 male). The Christian group included non-denominational, Catholic and Protestant Christians, while the non-religious group included participants that identified as agnostic, atheist or having no religion. Participants ranged in age from 18 years to 68 years old (*mean* = 33.92 years, *SD* = 10.35 years). The highest qualification of participants was primary school for two participants, high school for 49 participants, college for 45 participants, undergraduate university qualification for 87 participants, and a postgraduate or PhD qualification for 29 participants. Participants were recruited through the Prolific online participant pool, the experimental procedure took approximately an hour to complete, and each participant was reimbursed the equivalent of £9 for their time.

2.2. Study design

The full pre-registered study design, as well as data and reproducible code, are available through the Open Science Framework (OSF) project page (https://osf.io/sgv3h/). In order to address reviewer comments, we doubled the pre-registered sample size of this study. A complete summary of deviations from this pre-registration are available in the Supplementary Materials.

Participants were presented with descriptions of natural and supernatural phenomena and asked to provide what they consider to be the best explanation for each phenomenon. This allowed participants to explain the world in their own words, rather than through fixed scales or multi-choice responses.

There were 54 different descriptions of phenomena in the study, half of which referred to natural phenomena and half of which referred to supernatural phenomena (domain of phenomena). Here, ‘*natural*’ denotes parts of the Universe that are subject to the laws of nature and amenable to scientific analysis. ‘*Supernatural*’ denotes those parts of the Universe that are beyond the laws of nature and/or are not amenable to scientific analysis. We balanced the sentiment of phenomena being explained so that there was an even number of negative, neutral, and positive phenomena in each domain. We also split each domain into three further sub-domains, and asked participants to explain an equal number of phenomena for each sub-domain. For the natural domain, the three sub-domains were social, biological and physical phenomena. For the supernatural domain, the three sub-domains were traditional religious belief, superstition, and new age belief. In the Supplementary materials, we provide a full description of how sentiment and sub-domains of phenomena are defined, as well as additional analyses of their effects.

We anticipated that the study would require participants to concentrate for extended periods of time so only presented each participant with 36 of the 54 descriptions of phenomena in order to prevent fatigue. The order that phenomena were presented to participants was randomized. Participants were asked to give a written explanation for each of the 36 phenomena they were presented with. As part of the supplementary study, participants were also asked to specify the extent to which their explanation was natural and/or supernatural. Each phenomenon was presented on a separate page that included a text field and a prompt to provide an explanation. Explanations were constrained to be between 60 and 100 characters, which was enforced through the oTree software package used to run the study (Chen, Schonger, & Wickens, 2016).

At the end of the study, participants filled in a demographic survey, including age, educational level, gender, nationality and religious affiliation. In the post-experiment section participants were also asked to complete the Revised Paranormal Belief Scale (Tobacyk, 2004) which was used as an additional check on participants' religious and supernatural beliefs. A complete list of our pre-registered variables, models and hypotheses are available on the OSF project page.

2.3. Algorithm for calculating semantic similarity of explanations

We used a text-analytics approach to calculate a continuous measure of conceptual similarity between explanations. This avoided the subjectivity of manual coding, and enabled the quantitative analysis of free-text explanations on a scale not feasible using manual coding. All explanations were cleaned for comparison by removing all punctuation and stop-words (words that don't contain subject meaning) and converted to lower case. Remaining words were normalized to a common form through a process of lemmatization (Rinker, 2018). For example, *drive*, *drove*, and *driven* are all reduced to the common form *drive via* a dictionary lookup. This process results in a set of keywords for each explanation that can then be used in comparisons (Tonkin & Tourte, 2016). We used the R text-analytic packages *tm* and *textstem* for these processes (Feinerer & Hornik, 2008; Rinker, 2018).

We generated pairwise similarity measures between the keywords of all explanations for the same phenomena. Similarity between pairs of explanations was calculated using Jaccard index, defined as the number of unique overlapping keywords between the two explanations ($A \cap B$), divided by the total number of unique keywords ($A \cup B$) in the two explanations:

$$Jaccard\ index = \frac{|A \cap B|}{|A \cup B|}$$

where A indicates the set of keywords from one explanation and B indicates the set of words from a second explanation. Only explanations to the same phenomena were compared. If two sets contained exactly the same keywords, they would have a Jaccard similarity of 1. If two

explanations shared no common keywords the Jaccard similarity would be 0. This provided a general measure of the conceptual overlap between participants' explanations.

2.4. Variable transformations

Variables based on the features of participants, such as age, education, gender and religious affiliation, were transformed to pairwise comparisons representing the differences between participants. For example, for religious affiliation each pairwise comparison was classified as either; (1) proposed by two Christian participants; (2) proposed by one Christian and on non-religious participant; or (3) proposed by two non-religious participants. For continuous variables (e.g. *Age*) we used the absolute difference between participants. These variables were used to control for participant differences when modelling the similarity of explanations.

2.5. Modelling

We performed a series of analyses to test how religious affiliations and the domain of phenomena predict the similarity of participants' explanations. In these analyses we used mixed-effect models with three random effects: one random effect for the first participant being compared, one random effect for the second participant being compared, and one random effect for the specific phenomenon being explained. We also included control variables for age, gender and education. Additional models testing the frequency of supernatural explanations are reported in the Supplementary materials. The distribution of similarity scores was found to be exponentially patterned, so we used a GLMM with an exponential distribution to test our hypotheses. Analyses were implemented in the R v.3.5.2 programming environments (R Core Team, 2015) using the package MCMCglmm (Hadfield, 2010). Because this is a Bayesian framework, we focused on reporting the posterior distribution means, the 95% credibility intervals (CrI), and pMCMC. We ran all MCMCglmm analyses three times to ensure that the results were robust and all of our code is available on the OSF project page.

3. Results

3.1. Comparing the similarity of explanations within groups

To understand how homogeneous the explanations of Christian and non-religious people are, we tested whether Christian or non-religious people used more similar concepts to explain the world in general. Contrary to our predictions, we did not find evidence that Christians used more similar world explanations than non-religious people (*MCMCglmm:* posterior mean = −5.62, Credible Interval (*CrI*) = −31.31 to 21.32, *pMCMC* = 0.670), at least before the kind of phenomena being explained are taken into account (Supplementary Table 1). This runs contrary to the claim that Christianity functions to constrain and standardize people's global worldview.

Next, we tested whether the similarity of explanations within groups varied according to the domain of phenomena being explained. We hypothesized that Christians would propose more similar explanations for supernatural phenomena than natural phenomena, but that the explanations of non-religious people would not differ in similarity across domains. To test these predictions, we modelled the interaction between the religious affiliation of participants and the domain of phenomena being explained (Table 1). Contrary to our predictions, we found that Christian's explanations varied less than non-religious people's explanations across supernatural and natural phenomena (*MCMCglmm:* posterior mean = −60.91, *CrI* = −66.82 to −54.99, *pMCMC* < 0.001). Specifically, we found that non-religious participants proposed more similar explanations for natural phenomena than supernatural phenomena, whereas there was relatively little difference in the similarity of Christian's explanations across domains (Fig. 1). Our data suggests that there is greater diversity in the ways that non-religious participants explained the supernatural than in how they explained the natural world.

3.2. Between-group similarity of explanations

To understand whether people's religious affiliation was associated with the content of participants' explanations, we compared the similarity of explanations proposed by non-religious and Christian participants (between-group similarity) to the similarity of explanations within each group (Supplementary Table 2). In this section, we report two series of comparisons; one comparing the between-group similarity against the homogeneity of Christian's explanations, and one comparing the between-group similarity against the homogeneity of non-religious people's explanations.

Contrary to our predictions, we do not find evidence that Christian explanations were more similar than between-group explanations (*MCMCglmm*: posterior mean = −8.31, *CrI* = −21.90 to 4.48, *pMCMC* = 0.208). Neither did we find evidence that between-group explanation similarity was greater than the similarity of non-religious people's explanations (*MCMCglmm*: posterior mean = −1.75, *CrI* = −14.71 to 12.09, *pMCMC* = 0.814). While these results do not take into account how the similarity between Christian and non-religious people might vary across the kinds of phenomena being explained, they nevertheless suggest that religious affiliations do not strictly divide the way that people explain the world.

Next, we tested whether between-group similarity varies across the domains of phenomena being explained. This tests our prediction that Christians and non-religious people use more similar concepts when describing natural phenomena than supernatural phenomena.

First, we tested whether between-group similarity varied more across domains than the similarity of non-religious people's explanations (Supplementary Table 3). We find evidence that between-group similarity varies less across natural and supernatural phenomena than the similarity of non-religious people's explanations (*MCMCglmm*: posterior mean = 32.27, *CrI* = 27.68 to 37.22, *pMCMC* < 0.001). When explaining the natural world, between-group similarity was lower than the similarity of non-religious people's explanations (Fig. 1). When explaining supernatural phenomena, between-group similarity was higher than the similarity of non-religious people's explanations (Fig. 1). Counterintuitively, this indicates that, when explaining supernatural phenomena, non-religious people proposed explanations that shared more concepts with the explanations of Christians than other non-religious people. This may be because non-religious people used a similar base set of concepts as Christians, along with a heterogeneous range of other concepts.

We also tested whether between-group similarity varied more across domains than the similarity of Christian's explanations (Supplementary Table 3). We found that between-group similarity varied more across natural and supernatural phenomena than the similarity of Christian's explanations (*MCMCglmm*: posterior mean = −28.75, *CrI* = −34.24 to −23.40, *pMCMC* < 0.001). When explaining supernatural phenomena, between-group similarity was lower than the similarity of Christian's explanations (Fig. 1). When explaining natural phenomena, between-group similarity was close to the similarity of Christian's explanations (Fig. 1). This indicates that the concepts used by Christians to explain natural phenomena were largely overlapping with those used by non-religious people. Non-religious people proposed explanations that were based on a relatively narrow base of words, often involving science-based concepts (Supplementary Table 11). While Christians often refer to the same base concepts as non-religious individuals, some also use an expanded range of supernatural concepts. For example, when asked to explain why Earth's atmosphere contains oxygen and blocks UV radiation, a Christian participant responded “God created the earth as a home for humanity, the laws of nature in place keep the

Table 1
Summary of fixed effects for the model testing how religious affiliation and domain of phenomena predict similarity between explanations. For this model "Both non-religious" was set as the baseline level of Religion Comparison, and "Natural" was set at the baseline level for Subject Domain. Participant A, Participant B and Phenomena ID were included as random effects.

Predictor	Posterior distribution mean	Lower 95% CrI	Upper 95% CrI	Effective sample size	pMCMC
Religion comparison					
Different religions	18.06	5.70	32.39	1000.00	0.006
Both Christian	24.18	1.13	53.24	1199.13	0.052
Domain					
Supernatural	48.01	9.77	87.37	1000.00	0.014
Age difference	0.22	0.06	0.37	1000.00	0.008
Gender difference	3.27	1.40	5.55	884.80	< 0.001
Education difference	0.65	−0.70	2.11	854.53	0.356
Religion comparison: subject domain					
Different religions: supernatural	−32.30	−36.50	−27.55	1000.00	< 0.001
Both Christian: supernatural	−60.91	−66.82	−54.99	1000.00	< 0.001

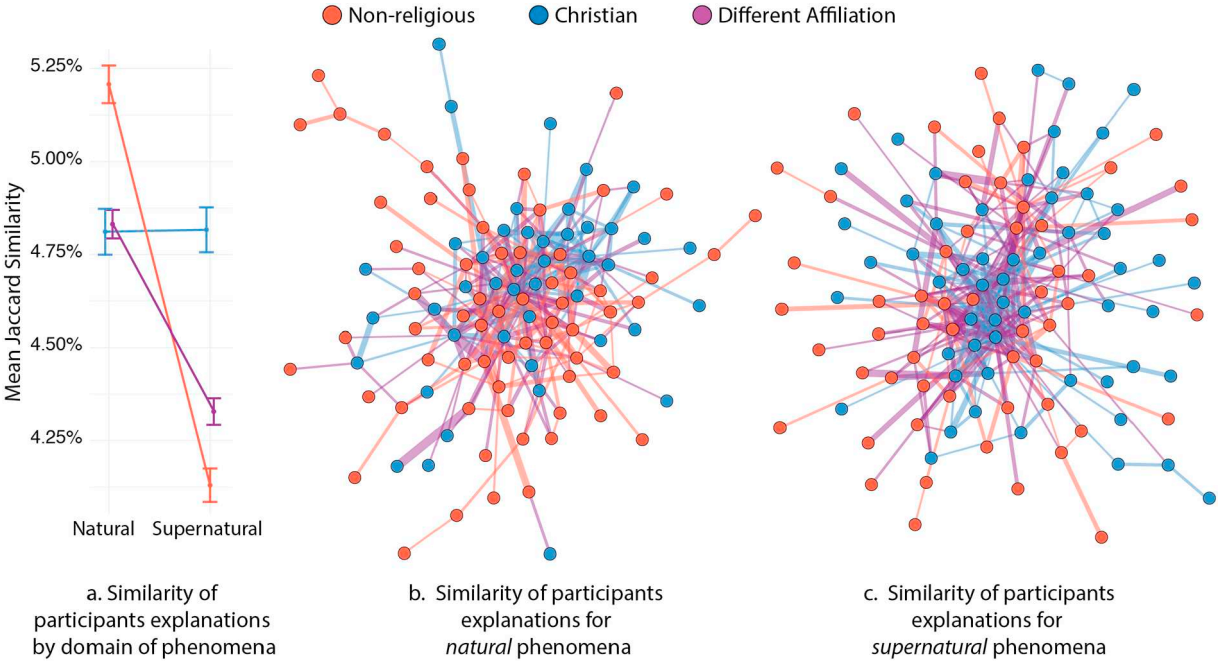

Fig. 1. Across all parts of the image, blue represents Christian participants, red indicates non-religious participants, and purple represents the relationship between Christian and non-religious participants. The line graph in part A represents the mean similarity of participant explanations by domain of phenomena. Error bars represent 95% confidence intervals. The networks illustrated in Parts B and C represent the mean similarity of participants' explanations for natural (Part B) and supernatural phenomena (Part C). The networks represent the strongest 300 links between participants, and participants not connected by any edges were removed from the network. The networks show only the participants that share the most similar explanations with others, and participants that propose more similar explanations to one another will tend to be closer together. Despite non-religious individuals proposing more similar explanations for natural phenomena, and Christians proposing more similar explanations for supernatural phenomena, there is substantial overlap between the concepts used by Christian and non-religious people across both networks. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

balance." This illustrates how Christian worldviews can synthesize science-based and religious-based concepts (Evans & Lane, 2011; Legare & Visala, 2011; Watts, 1997).

3.3. Testing the validity of Jaccard similarity

Inspection of our data showed that overlap in concepts did not always strictly indicate agreement between participants. For example, when explaining supernatural phenomena, the explanations proposed by non-religious participants sometimes contained negations, qualification, or implied a lacked endorsement. When asked to explain the contents of the Bible, a non-religious participant wrote "The Bible's point is to guide people to a good life, no matter how or by whom it was written." This highlights one of the limitations of using Jaccard similarity: while this measure of similarity gets at the broad conceptual overlap in explanations, it does not always capture the subtleties expressed in language.

To check the validity of our methodological approach, we performed a follow-up study testing whether Jaccard similarity reliably corresponds to human coder's perception of similarity (Supplementary Study B). In the follow up study, we had 100 additional participants rate the similarity of a subset of explanations proposed in the main study. Participants were presented two explanations for the same phenomena and asked to rate the similarity of these explanations on a Likert scale of 0 (Very different) to 10 (Very similar). We then tested whether the human coder's ratings of similarity predicted our automated Jaccard similarity measure. Our results show that human similarity ratings significantly predicted Jaccard Similarity (*MCMCglmm*: posterior mean = −8.70, *CrI* = −11.70 to −5.67, *pMCMC* < 0.001), indicating that Jaccard similarity generally corresponds to how people perceive the similarity of different explanations.

3.4. Additional analyses

We performed additional analyses to test whether participants self-identified affiliation of Christian and non-religious correspond to differences in commitments to supernatural beliefs. All participants in the main study completed the Revised Paranormal Belief Scale, and we used the Traditional Religious Belief dimension as a measure of Christian belief (Tobacyk, 2004). We found that Christians have greater commitment to Traditional Religious Beliefs ($Mdn = 5.75$) than non-religious participants ($Mdn = 1.25$), $W = 10{,}822$, $p < .001$ (Supplementary Table 15). This indicates that there are clear differences in the commitment of our non-religious and Christian participants to traditional religious beliefs (Supplementary Fig. 5).

In the Supplementary Methods section, we also report the results of further analyses testing how the sentiment of phenomena and the specific sub-domain of phenomena predict the similarity of participants' explanations (Supplementary Tables 4–9).

4. Discussion

Our findings challenge the popular claim that religious system homogenize people's worldviews in general (Dawkins, 2006; Dennett, 2006). Instead, we find that the homogeneity of Christian and non-religious people's explanations depends on the kind of phenomena being explained. Christians proposed more homogenous explanations than non-religious people for supernatural phenomena, but not natural phenomena. When explaining the natural world, Christian and non-religious people primarily drew on science-based concepts, with some Christians supplementing these concepts with religious-based concepts. When explaining supernatural phenomena, Christians drew on a shared set of religious-based concepts, but non-religious people lacked a common conceptual framework and showed relatively little consensus in their explanations. This suggests that Christianity primarily provides a common conceptual framework for supernatural phenomena and that non-religious people have a diverse range of perspectives on the supernatural.

We also found substantial overlap in the concepts used by Christian and non-religious people. When explaining supernatural phenomena, non-religious people proposed explanations that, on average, shared more concepts with Christians than they did with other non-religious people. When explaining the natural world, the explanations proposed by Christians shared a similar number of concepts to the explanations of other Christians as they did to the explanations of non-religious people. Consistent with the predictions of synthesis-based accounts, this suggests that the primary difference between religious and secular worldviews is in the scope of concepts drawn upon, rather than the core concepts (Legare & Visala, 2011; Watson-Jones, Busch, & Legare, 2015). This challenges the idea that religious and secular worldviews are necessarily competing and demonstrates how text analytics can efficiently quantify the structure and diversity of group ideologies.

CRediT authorship contribution statement

Joseph Watts: Conceptualization, Data curation, Formal analysis, Funding acquisition, Investigation, Methodology, Visualization, Writing - original draft. **Sam Passmore:** Conceptualization, Methodology, Data curation, Formal analysis, Writing - review & editing. **Joshua Conrad Jackson:** Writing - review & editing. **Christoph Rzymski:** Methodology, Writing - review & editing. **Robin I. Dunbar:** Funding acquisition, Writing - review & editing, Supervision.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.cognition.2020.104290.

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